

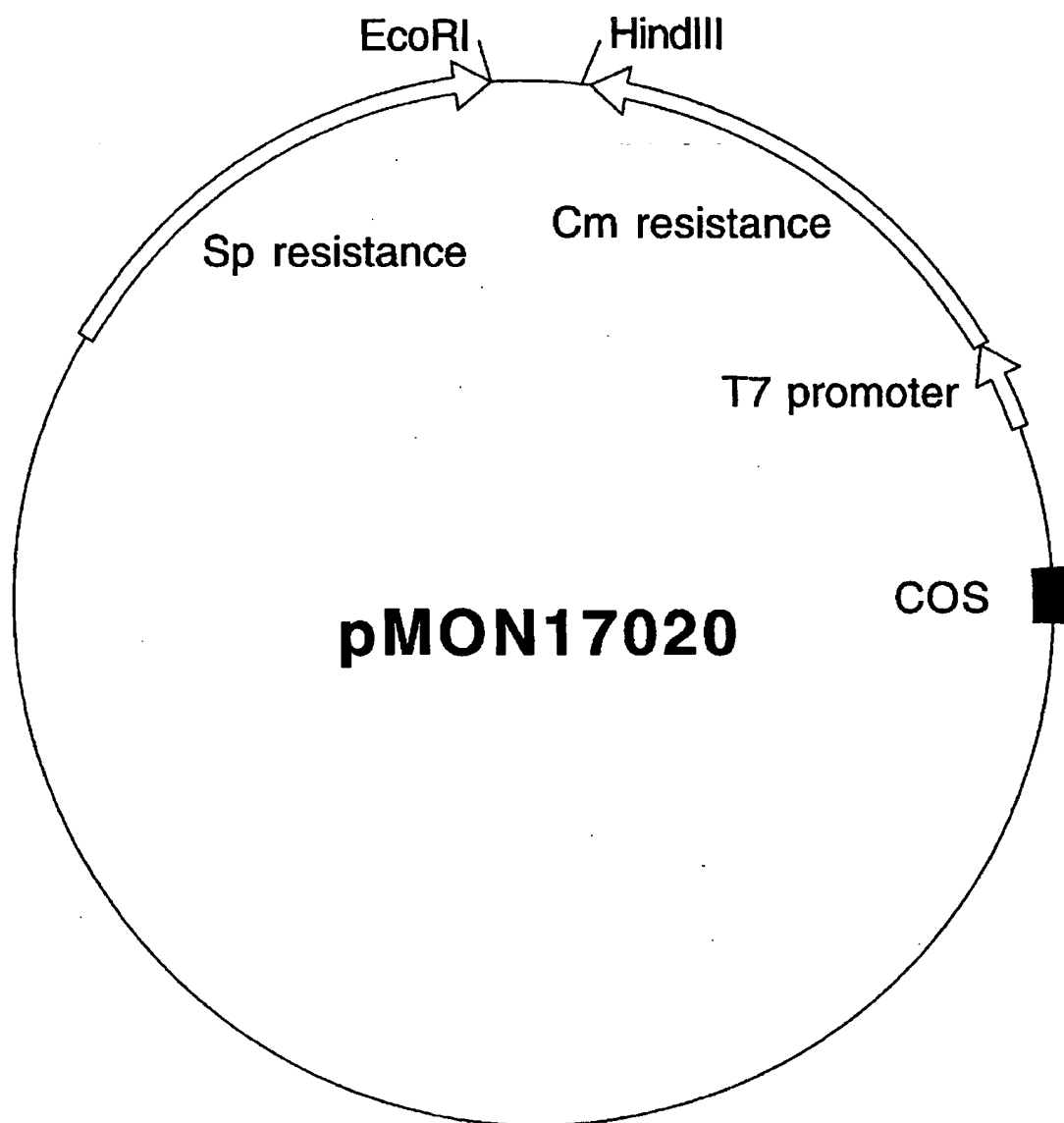
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TCATCAAAATATTTAGCAGCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATC 6417  
6358 AGTAGTTTATAAATCGTCGTAAGGTCTAACCCTAAGTTAGTTGTTCCATGCTCGGTATAG  
ACTTTATTCAAAATTGGTATCGCCAAAAACCAAGAAGAACTCCCATCCTCAAAAGGTTTGTA 6477  
6418 TGAAATAAGTTTAACCATAGCGGTTTGTGTTCTTCCCTTGAGGTAGGAGTTTCCAAACAT  
AGGAAGAAATTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTA 6537  
6478 TCCTTCTTAAGAGTCAGGTTTCGGAGTTGTGTTCCAGTCCCATGTCTCAGAGGTTTGGTAAT  
GCCAAAAGCTACAGGAGATCAATGAAGAAATCTTCAATCAAAAGTAAACTACTGTTCAGCA 6597  
6538 CGGTTTTTCGATGTCCCTCTAGTTACTTCTTAGAAGTTAGTTTTCATTTTGATGACAAGGTCGT  
CATGCATCATGGTCAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGG 6657  
6598 GTACGTAGTACCAGTCATTCAAAAGTCTTTTCTGTAGGTGGCTTCTGAATTTCAATCACC

Figure 1A

6658 GCATCTTTGAAAGTAAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACGACAGACAAAAA 6717  
CGTAGAAACTTTTCATTAGAACAGTTGTAGCTCGTCGACCGAACACCCCTGGTCTGTGTTTT  
6718 AGGAATGGTGCAGAAATTGTTAGGCGCACCTACCAAAGCATCTTTGCCCTTTATTGCAAAAG 6777  
TCCTTACCACGCTTTAAACAAATCCGCGTGGATGGTTTTTCGTAGAAACGGAAATAACGTTTC  
6778 ATAAAGCAGATTCCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCCCTG 6837  
TATTTCTAAGGAGATCATGTTCAACCCCTTGTTTTTATTGTCACCTTTTCTCGACAGGAC  
6838 ACAGCCCACTCACTAATGCGTATGACGAACGCAGTGACGACCACAAAGAAATTCCTCTCTA 6897  
TGTCGGGTGAGTGATTACGCATACTGCTTGCGTCACTGCTGGTGTGTTCTTAAGGGAGAT  
TATAAGAAGGCATTCAATCCCATTTGAAGGATCATCAGATACTAACCAATATTTCTC  
6898 ATATTCTCCGTAAGTAAGGGTAAACTTCCTAGTAGTCTATGATTGGTTATAAAGAG 6954

sspl

Figure 1B

**Figure 2**

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AAGCCCGCGT TCTCTCCGGC GCTCCGCCCG GAGAGCCGTG GATAGATTAA GGAAGACGCC 60
C   ATG TCG CAC GGT GCA AGC AGC CGG CCC GCA ACC GCC CGC AAA TCC 106
    Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser 15
      1      5      10
TCT GGC CTT TCC GGA ACC GTC CGC ATT CCC GGC GAC AAG TCG ATC TCC 154
Ser Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser 30
      20      25
CAC CGG TCC TTC ATG TTC GGC GGT CTC GCG AGC GGT GAA ACG CGC ATC 202
His Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile 45
      35      40
ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC AAT ACG GGC AAG GCC ATG 250
Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met 60
      50      55
CAG GCC ATG GGC GCC AGG ATC CGT AAG GAA GGC GAC ACC TGG ATC ATC 298
Gln Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile 75
      65      70
GAT GGC GTC GGC AAT GGC GGC CTC CTG GCG CCT GAG GCG CCG CTC GAT 346
Asp Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp 95
      80      85

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Figure 3A

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      16600
      16610
      16620
      1663
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CAG GGC TTT GGC GCC AAC CTT ACC GTC GAG ACG GAT GCG GAC GGC GTG	730
Gln Gly Phe Gly Ala Asn Leu Thr Val Gln Thr Asp Ala Asp Gly Val	
210	
CGC ACC ATC CGC CTG GAA GGC CGC GGC AAG CTC ACC GGC CAA GTC ATC	778
Arg Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile	
225	
230	
235	
GAC GTG CCG GGC GAC CCG TCC TCG ACG GCC TTC CCG CTG GTT GCG GCC	826
Asp Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala	
240	
245	
250	
255	
CTG CTT GTT CCG GGC TCC GAC GTC ACC ATC CTC AAC GTG CTG ATG AAC	874
Leu Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn	
260	
265	
270	
CCC ACC CGC ACC GGC CTC ATC CTG ACG CTG CAG GAA ATG GGC GCC GAC	922
Pro Thr Arg Thr Gly Leu Ile Leu Thr Thr Leu Gln Glu Met Gly Ala Asp	
275	
280	
285	
ATC GAA GTC ATC AAC CCG CGC CTT GCC GGC GGC GAA GAC GTG GCG GAC	970
Ile Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp	
290	
295	
300	
CTG CGC GTT CGC TCC ACC CTG AAG GGC GTC ACG GTG CCG GAA GAC	1018
Leu Arg Val Arg Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp	
305	
310	
315	

Figure 3C

CGC GCG CCT TCG ATG ATC GAC GAA TAT CCG ATT CTC GCT GTC GCC GCC 1066  
Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala 335  
320 325

GCC TTC GCG GAA GGG GCG ACC GTG ATG AAC GGT CTG GAA GAA CTC CGC 1114  
Ala Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg 350  
340 345

GTC AAG GAA AGC GAC CGC CTC TCG GCC GTC GCC AAT GGC CTC AAG CTC 1162  
Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu 365  
355 360

AAT GGC GTG GAT TGC GAT GAG GGC GAG Glu Gly Thr Ser Leu Val Val Arg Gly 1210  
Asn Gly Val Asp Cys Asp Glu Gly 375 380

CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GTC GCC 1258  
Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala 395  
385 390

ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC 1306  
Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu 415  
400 405

GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG 1354  
Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr 430  
420 425

Figure 3D

AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC 1402  
Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile 445  
435 440  
GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGGTC 1456  
Glu Leu Ser Asp Thr Lys Ala Ala 455  
450  
CCGCTGCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTTTCATC 1516  
ATCTCGATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCTGT 1576  
CGCTTGATGA CGAGGCGGTT GCGGCCGATG TCGCCCCGAA TCTCGATCTT GCCGGGCTCG 1636  
ACCGGTCGGT GCTGTGCGGC CATGCCATCG GCGAGGCGGC TTCGAAGATC GCGGTCATGC 1696  
CCTCGGTGCG GCGGGCGCTG GTCGAGGCGC AGCGCAGCTT TCGGCGCGT GAGCCGGGCA 1756  
CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCCC GGATGCGCCG GTGAAAGCTCT 1816  
ATGTCACCGC GTCACCGGAA GTGCGCGCGA AACGCCGCTA TGACGAAATC CTCGGCAAATG 1876  
GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA 1936  
TGGGTGCGGC GGACAGTCCT TTGAAGCCCCG CCGACGATGC GCACCTT 1982

**Figure 3E**



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GTAGCCACAC ATAATTACTA TAGCTAGGAA GCCCGCTATC TCCTCAATCCC GCGTGATCGC 60
GCCAAAATGT GACTGTGAAA AATCC ATG TCC CAT TCT GCA TCC CCG AAA CCA 112
Met Ser His Ser Ala Ser Pro Lys Pro
1 5
GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC ATT CCG 160
Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
10 15 20 25
GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT CTC GCA 208
Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
30 35 40
TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC 256
Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
45 50 55
AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCC GCG AAA ATC CGT AAA GAG 304
Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
60 65 70
GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG TTG CAG 352
Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
75 80 85

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Figure 4A

400 CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG CGC CTC  
 Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu  
 90 95 100 105  
 448 ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT ATC GGC  
 Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly  
 110 115 120  
 496 GAC GCC TCG CTG TCG AAG CGC CCG ATG GGC CGC GTG CTG AAC CCG TTG  
 Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu  
 125 130 135  
 544 CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC ATG CCG  
 Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro  
 140 145 150  
 592 CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT CGC GTG  
 Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr Arg Val  
 155 160 165  
 640 CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC GGT CTC  
 Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Ala Gly Leu  
 170 175 180 185  
 688 AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC CGC GAC  
 Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr Arg Asp  
 190 195 200

Figure 4B

CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG GTC GAG 736  
His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu 215  
205 210

ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG GGC AAG 784  
Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys 230  
220 225

CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG ACC GCC 832  
Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala 245  
235 240

TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC ACC ATC 880  
Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val Thr Ile 260  
250 255

CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC ACC TTG 928  
Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu 275  
270

CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT GCA GGC 976  
Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly 290  
285 295

GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC AAG GGC 1024  
Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly 300  
305 310

Figure 4C

GTC GTC GTT CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA TAT CCG Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro 315 320	1072
GTC CTG GCG ATT GCC GCC TCC TTC GCG GAA ACC GTG ATG GAC Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val Met Asp 330 335	1120
GGG CTC GAC GAA CTG CCG GTC AAG GAA TCG GAT CGT CTG GCA GCG GTC Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Val 350 355	1168
GCA CGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC GAG ATG Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly Glu Met 365 370	1216
TCG CTG ACG GTT CGC GCG CGC CCC GAC GGC AAG GGA CTG GCG GGC GGC Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly Gly Gly 380 385	1264
ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC CTC GTG Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val 395 400	1312
ATG GGC CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT AAC ATG Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser Asn Met 410 415	1360

Figure 4D

ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC	1408
Ile Ala Thr Ser Phe Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly	
430 435 440	
GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAATA TATTATTTC	1462
Ala Lys Ile Glu Leu Ser Ile Leu	
445	
GAGATTGGGC ATTATTACCG GTTGTCTCA GCGGGGGTTT AATGTCCAAT CTTCCATACG	1522
TAACAGCATC AGGAAATATC AAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCGC	1582
CTAAGCTTTC TCAAGACTTC GTTAAAACTG TACTGAAATC CCGGGGGGTC CCGGGATCAA	1642
ATGACTTCAT TTCTGAGAAA TTGGCCTCGC A	1673

Figure 4E

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54      GTGATCGCGC CAAAATGTGA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG
          Met Ser His Ser Ala Ser Pro
          1           5

102     AAA CCA GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC
          Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg
          10      15      20

150     ATT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT
          Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly
          25      30      35

198     CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC
          Leu Ala Ser Gly Glu Thr Arg Thr Thr Gly Leu Glu Gly Glu Asp
          40      45      50      55

246     GTC ATC AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT
          Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg
          60      65      70

294     AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG
          Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu
          75      80      85

342     TTG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG
          Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala
          90      95      100

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Figure 5A

CGC CTC ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT	390
Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe	
105 110 115	
ATC GGC GAC GCC TCG CTG TCG AAG CGC CCG ATG GGC CGC GTG CTG AAC	438
Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn	
120 125 130 135	
CCG TTG CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC	486
Pro Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg	
140 145 150	
ATG CCG CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT	534
Met Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr	
155 160 165	
CGC GTG CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC	582
Arg Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala	
170 175 180	
GGT CTC AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC	630
Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr	
185 190 195	
CGC GAC CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG	678
Arg Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr	
200 205 210 215	

Figure 5B

726  
GTC GAG ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG  
Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln  
220 225 230

774  
GGC AAG CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG  
Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser  
235 240 245

822  
ACC GCC TTC CCG CTC GGT GGC GCC CTT CTG GTG GAA GGT TCC GAC GTC  
Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val  
250 255 260

870  
ACC ATC CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC  
Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu  
265 270 275

918  
ACC TTG CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT  
Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu  
280 285 290 295

966  
GCA GGC GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC  
Ala Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu  
300 305 310

1014  
AAG GGC GTC GTC GTT CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA  
Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu  
315 320 325

Figure 5C



1062  
 TAT CCG GTC CTG GCG ATT GCC GCC TTC GCG GAA GGC GAA ACC GTG  
 Tyr Pro Val 330  
 335  
 340  
 1110  
 ATG GAC GGG CTC GAC GAA CTG CGC GTC AAC GAA TCG GAT CGT CTG GCA  
 Met Asp Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala  
 345  
 350  
 355  
 1158  
 GCG GTC GCA CGC GGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC  
 Ala Val Ala Arg Gly Leu 365  
 360  
 370  
 375  
 1206  
 GAG ATG TCG CTG ACG GTT CGC GGC CGC CCC GAC GGC AAG GGA CTG GGC  
 Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly  
 380  
 385  
 390  
 1254  
 GGC GGC ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC  
 Gly Gly Thr Val 395  
 400  
 405  
 1302  
 CTC GTG ATG GGC CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT  
 Leu Val Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser  
 410  
 415  
 420  
 1350  
 AAC ATG ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA  
 Asn Met Ile Ala Thr Ser Phe Pro Glu Phe Met Met Met Pro Gly  
 425  
 430  
 435

Figure 5D

TTG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA	1400
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu	
440	
445	
TATTATTGCG GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT	1460
CTTCCATACG TAACAGCATC AGGAAATATC AAAAAGCTT	1500

**Figure 5E**



248 TAFPLVAALLVPGSDVTILNVLMNPTRTGLILT..LQEMGADIEVINPRL 295  
  . | : : | | : : | : | : : : : : | : : | | | | |  
245 SASYFLAAAIKGGTVKVTGIGRNSMQDIRFADVLEKMGATI..... 287

296 AGGEDVADLRVRSSTLKGVTPEDRAPSMIDEYPILAVAAFAEGATVMN 345  
  . | : | : : . . . : : : : | . : : | | | | | : :  
288 CWGDDY..ISCTRGELNAIDMDMNHIP...DAAMTIAAALFAKGTTTLR 332

346 GLEELRVKESDRLSAVANGLKLVGDCDEGETSLVVRGRPDGKGLGNASG 395  
  : : : | | | | | | : : : : : : : : : : : : : : : :  
333 NIYNWRVKETDRRLFAMATELRKVGAEVEEGHDYIRI.TPPEKLN..... 376

396 AAVATHLDHRIAMSFVLMGLVSENVPVTVDDATMIATSFPEFMDLMAGLGA 445  
  | : : | | | : : | : : | : : | : : | : : | : : | : : : : : : : : : :  
377 AEIATYNDHRMAMCFSLVAL.SDTPVTILDPKCTAKTFPDYFEQLARISQ 425

446 KIELSDTKAA\* 456

426 AA\*..... 428

Figure 6B



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301 VADLRVRSSTLKGVTVPEDRAPSMID EY P I L A V A A A F A E G A T V M N G L E E L 350
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 VADLRVRASKLKGVVPPERAPSMID EY P V L A I A A S F A E G E T V M D G L D E L 350

351 RVKESDRLS A V A N G L K L N G V D C D E G E T S L V V R G R P D G K G L G N A S G A A V A T 400
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 RVKESDRLA A V A R G L E A N G V D C T E G E M S L T V R G R P D G K G L G . . . G G T V A T 397

401 HLDHRIAMS F L V M G L V S E N P V T V D D A T M I A T S F P E F M D L M A G L G A K I E L S 450
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
398 HLDHRIAMS F L V M G L A A E K P V T V D D S N M I A T S F P E F M D M P G L G A K I E L S 447

451 DTKAA* 456

448 IL.... 449

```

# Figure 7B

60 CCATGGCTCA CGGTGCAAGC AGCCGTCCAG CAACTGCTCG TAAGTCCTCT GGTCTTTCTG  
120 GAACCGTCCG TATTCCAGGT GACAAGTCTA TCTCCACAG GTCCTTCATG TTTGGAGGTC  
180 TCGCTAGCGG TGAAACTCGT ATCACCGGTC TTTTGGGAAGG TGAAGATGTT ATCAACACTG  
240 GTAAGGCTAT GCAAGCTATG GGTGCCAGAA TCCGTAAAGGA AGGTGATACT TGGATCATTG  
300 ATGGTGTGG TAACGGTGA CTCCTTGCTC CTGAGGCTCC TCTCGATTTC GGTAACGCTG  
360 CAACTGGTTG CCGTTTGACT ATGGGTCTTG TTGGTGTTTA CGATTTCGAT AGCACTTTCA  
420 TTGGTGACGC TTCTCTCACT AAGCGTCCAA TGGGTCGTGT GTTGAACCCCA CTTCGCGAAA  
480 TGGGTGTGCA GGTGAAGTCT GAAGACGGTG ATCGTCTTCC AGTTACCTTG CGTGGACCAA  
540 AGACTCCAAAC GCCAATCACC TACAGGGTAC CTATGGCTTC CGCTCAAGTG AAGTCCGCTG  
600 TTCTGCTTGC TGGTCTCAAC ACCCCAGGTA TCACCACTGT TATCGAGCCA ATCATGACTC  
660 GTGACCACAC TGAAAAGATG CTTCAAGGTT TTGGTGCTAA CCTTACCGTT GAGACTGATG  
720 CTGACGGTGT GCGTACCATC CGTCTTGAAG GTCGTGGTAA GCTCACCGGT CAAGTGATTG  
780 ATGTTCCAGG TGATCCATCC TCTACTGCTT TCCCATTGGT TGCTGCCCTG CTTGTTCCAG  
840 GTTCCGACGT CACCATCCTT AACGTTTGA TGAACCCAAC CCGTACTGGT CTCATCTTGA

**Figure 8A**

CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGAGAAG	900
ACGTGGCTGA CTTCGGTGTT CGTCTTCTA CTTTGAAGGG TGTACTGTT CCAGAAGACC	960
GTGCTCCCTC TATGATCGAC GAGTATCCAA TTCTCGCTGT TGCAGCTGCA TTCGCTGAAG	1020
GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGTGTAA GGAAAGCGAC CGTCTTCTG	1080
CTGTCGCAA CCGTCTCAAG CTCAACGGTG TTGATTGCGA TGAAGGTGAG ACTTCTCTCG	1140
TCGTGCGTGG TCGTCCCTGAC GGTAAGGGTC TCGGTAAACGC TTCTGGAGCA GCTGTCGCTA	1200
CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGAAAACC	1260
CTGTTACTGT TGATGATGCT ACTATGATCG CTACTAGCTT CCCAGAGTTC ATGGATTGA	1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC	1377

**Figure 8B**



AGATCTATCG	ATAAGCTTGA	TGTAATTGGA	GGAAGATCAA	AATTTTCAAT	CCCCATTCTT	60
CGATTGCTTC	AATTGAAGTT	TCTCCG	ATG GCG CAA	GTT AGC AGA	ATC TGC AAT	113
	Met	Ala	Gln	Val	Ser Arg Ile Cys Asn	
	1			5		
GGT GTG	CAG AAC	CCA TCT	CTT ATC	TCC AAT	CTC TCG AAA	TCC AGT CAA
Gly Val	Gln Asn	Pro Ser	Leu Ile	Ser Asn	Leu Ser	Lys Ser Ser Gln
10		15			20	25
CGC AAA	TCT CCC	TTA TCG	GTT TCT	CTG AAG	ACG CAG	CAT CCA CGA
Arg Lys	Ser Pro	Leu Ser	Val Ser	Leu Lys	Thr Gln	His Pro Arg
	30			35		40
GCT TAT	CCG ATT	TCG TCG	TCG TCG	TGG GGA	TTG AAG	AAG AGT GGG
Ala Tyr	Pro Ile	Ser Ser	Ser Trp	Gly Leu	Lys Lys	Ser Gly Met Thr
	45			50		55
TTA ATT	GGC TCT	GAG CTT	CGT CCT	CTT AAG	GTC ATG	TCT TCT GTT
Leu Ile	Gly Ser	Glu Leu	Arg Pro	Leu Lys	Val Met	Ser Ser Val Ser
	60			65		70
ACG GCG	TGC ATG	C				
Thr Ala	Cys Met					
	75					

Figure 9

AGATCTATCG	ATAAGCTTGA	TGTAATTGGA	GGAAGATCAA	AATTTTCAAT	CCCCATTCTT	60
CGATTGCTTC	AATTGAAGTT	TCTCCG	ATG GCG CAA GTT AGC AGA ATC TGC AAT			113
			Met Ala Gln Val Ser Arg Ile Cys Asn			
			1	5		
GGT GTG CAG AAC CCA TCT CTT ATC TCC AAT CTC TCG AAA TCC AGT CAA						161
Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln						
10	15	20	25			
CGC AAA TCT CCC TTA TCG GTT TCT CTG AAG ACG CAG CAT CCA CGA						209
Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg						
30	35	40				
GCT TAT CCG ATT TCG TCG TCG TGG GGA TTG AAG AAG AGT GGG ATG ACG						257
Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys Ser Gly Met Thr						
45	50	55				

# Figure 10A

TTA	ATT	GGC	TCT	GAG	CTT	CGT	CCT	CTT	AAG	GTC	ATG	TCT	TCT	GTT	TCC	305
Leu	Ile	Gly	Ser	Glu	Leu	Arg	Pro	Leu	Lys	Val	Met	Ser	Ser	Val	Ser	
		60					65					70				
ACG	GCG	GAG	AAA	GCG	TCG	GAG	ATT	GTA	CTT	CAA	CCC	ATT	AGA	GAA	ATC	353
Thr	Ala	Glu	Lys	Ala	Ser	Glu	Ile	Val	Leu	Gln	Pro	Ile	Arg	Glu	Ile	
		75				80					85					
TCC	GGT	CTT	ATT	AAG	TTG	CCT	GGC	TCC	AAG	TCT	CTA	TCA	AAT	AGA	ATT	401
Ser	Gly	Leu	Ile	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg	Ile	
90					95					100					105	
C																402

Figure 10B

AGATCTTCA AGA ATG GCA CAA ATT AAC AAC ATG GCT CAA GGG ATA CAA	49
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln	
1 5 10	
ACC CTT AAT CCC AAT TCC AAT TTC CAT AAA CCC CAA GTT CCT AAA TCT	97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser	
15 20 25	
TCA AGT TTT CTT GTT TTT GGA TCT AAA AAA CTG AAA AAT TCA GCA AAT	145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn	
30 35 40	
TCT ATG TTG GTT TTG AAA AAA GAT TCA ATT TTT ATG CAA AAG TTT TGT	193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys	
45 50 55 60	
TCC TTT AGG ATT TCA GCA TCA GTG GCT ACA GCC TGC ATG C	233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met	
65 70	

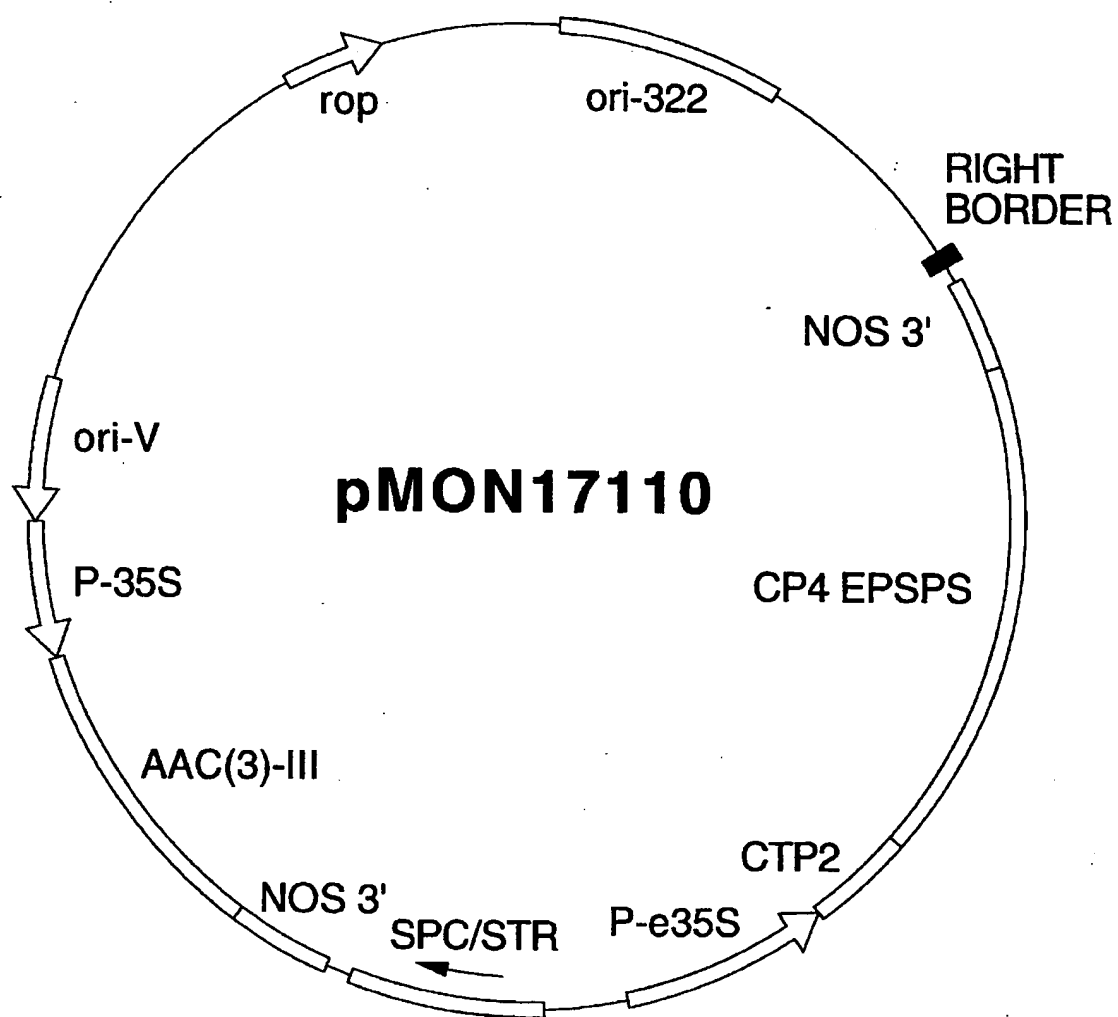
Figure 11

AGATCTGCTA GAAATAATTT TGTTTAACTT TAAGAAGGAG ATATATCC ATG GCA CAA	57
Met Ala Gln	
1	
ATT AAC AAC ATG GCT CAA GGG ATA CAA ACC CTT AAT CCC AAT TCC AAT	105
Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn	
5 10 15	
TTC CAT AAA CCC CAA GTT CCT AAA TCT TCA AGT TTT CTT GTT TTT GGA	153
Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu Val Phe Gly	
20 25 30 35	
TCT AAA AAA CTG AAA AAT TCA GCA AAT TCT ATG TTG GTT TTG AAA AAA	201
Ser Lys Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys	
40 45 50	

**Figure 12A**

GAT TCA ATT TTT ATG CAA AAG TTT TGT TCC TTT AGG ATT TCA GCA TCA	249
Asp Ser Ile Phe 55 Met Gln Lys Phe Cys Ser Phe Arg Ile Ser Ala Ser	60
	65
GTG GCT ACA GCA CAG AAG CCT TCT GAG ATA GTG TTG CAA CCC ATT AAA	297
Val Ala Thr Ala 70 Gln Lys Pro Ser Ser Glu Ile Val Leu Gln Pro Ile Lys	75
	80
GAG ATT TCA GGC ACT GTT AAA TTG CCT GGC TCT AAA TCA TTA TCT AAT	345
Glu Ile Ser Gly Thr Val Lys Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn	85
	90
	95
AGA ATT C	352
Arg Ile	
100	

Figure 12B

**Figure 13**

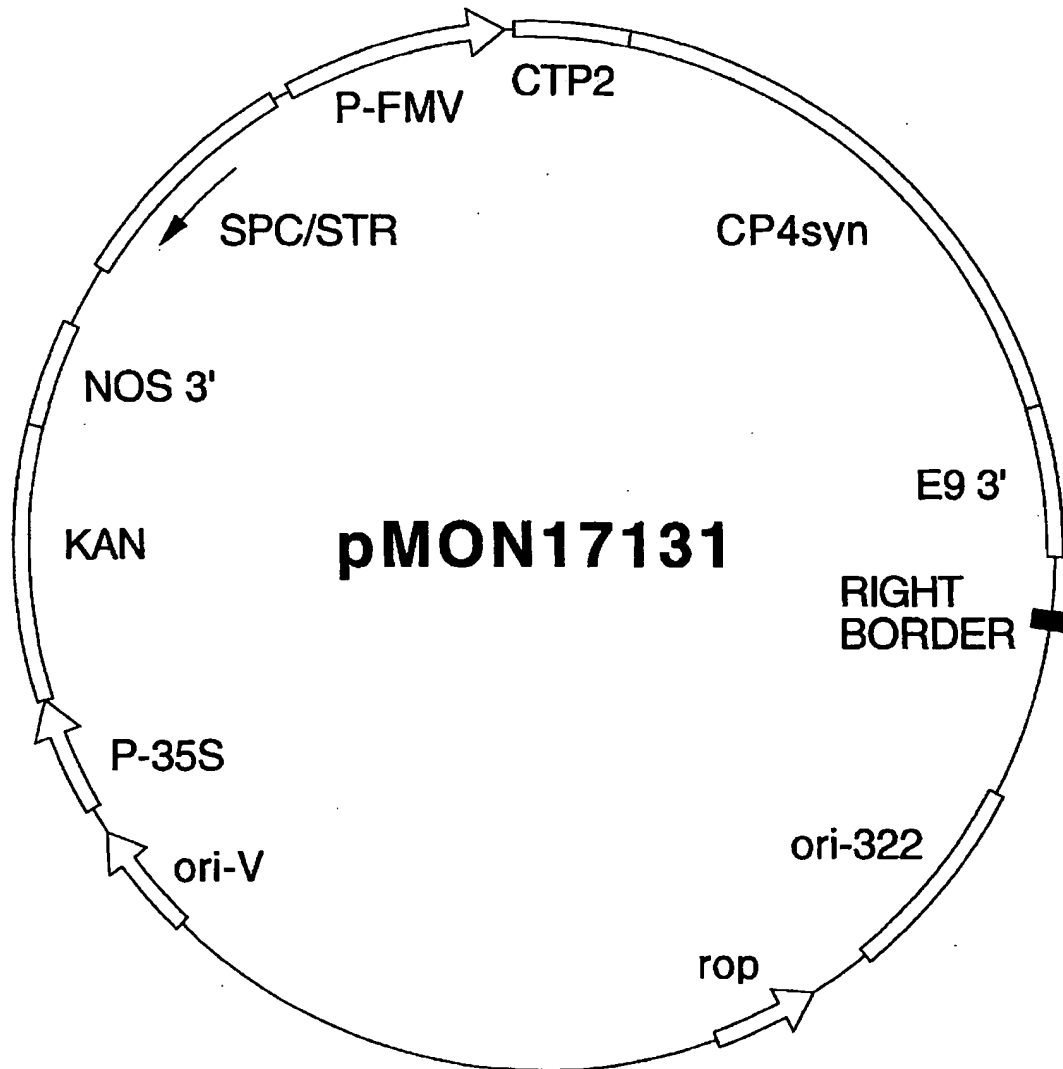
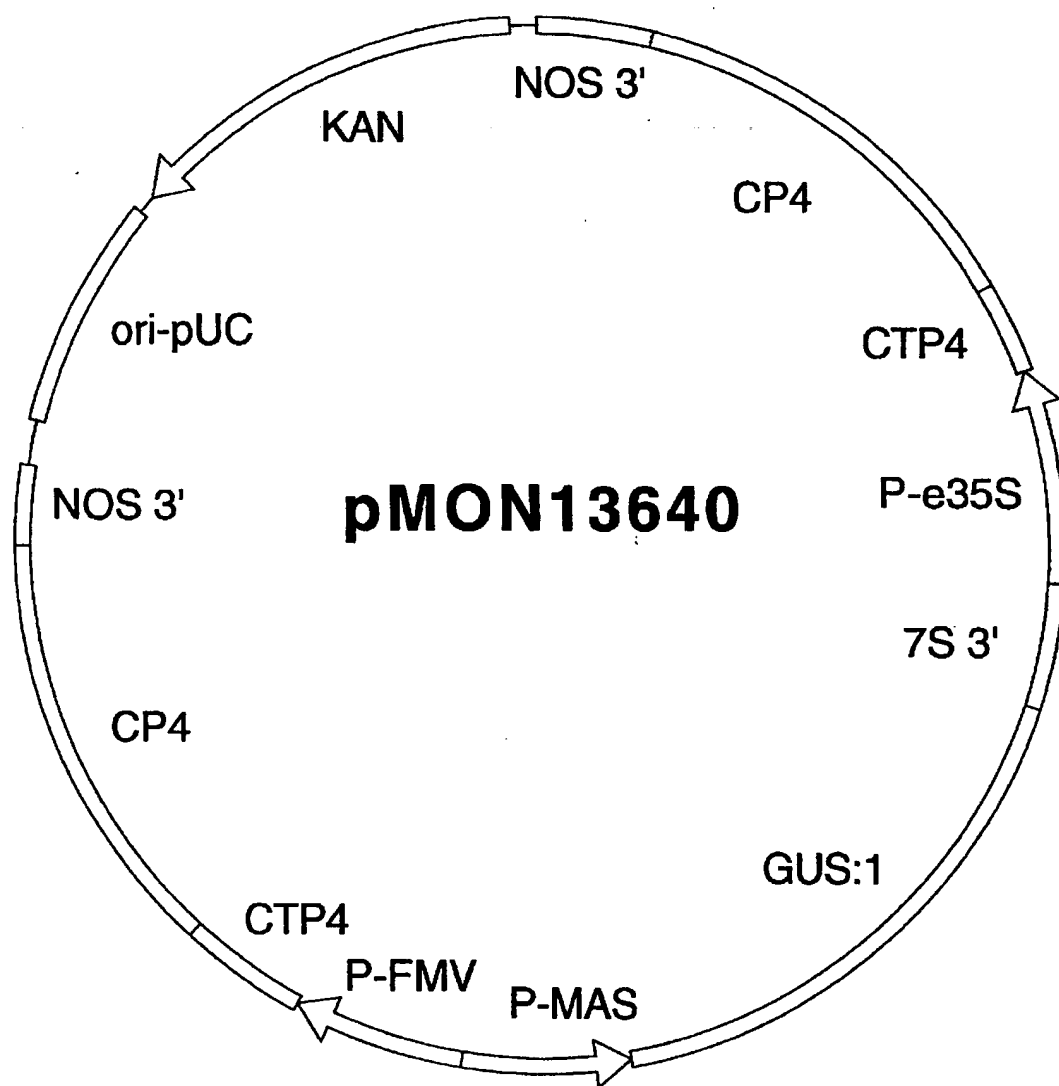
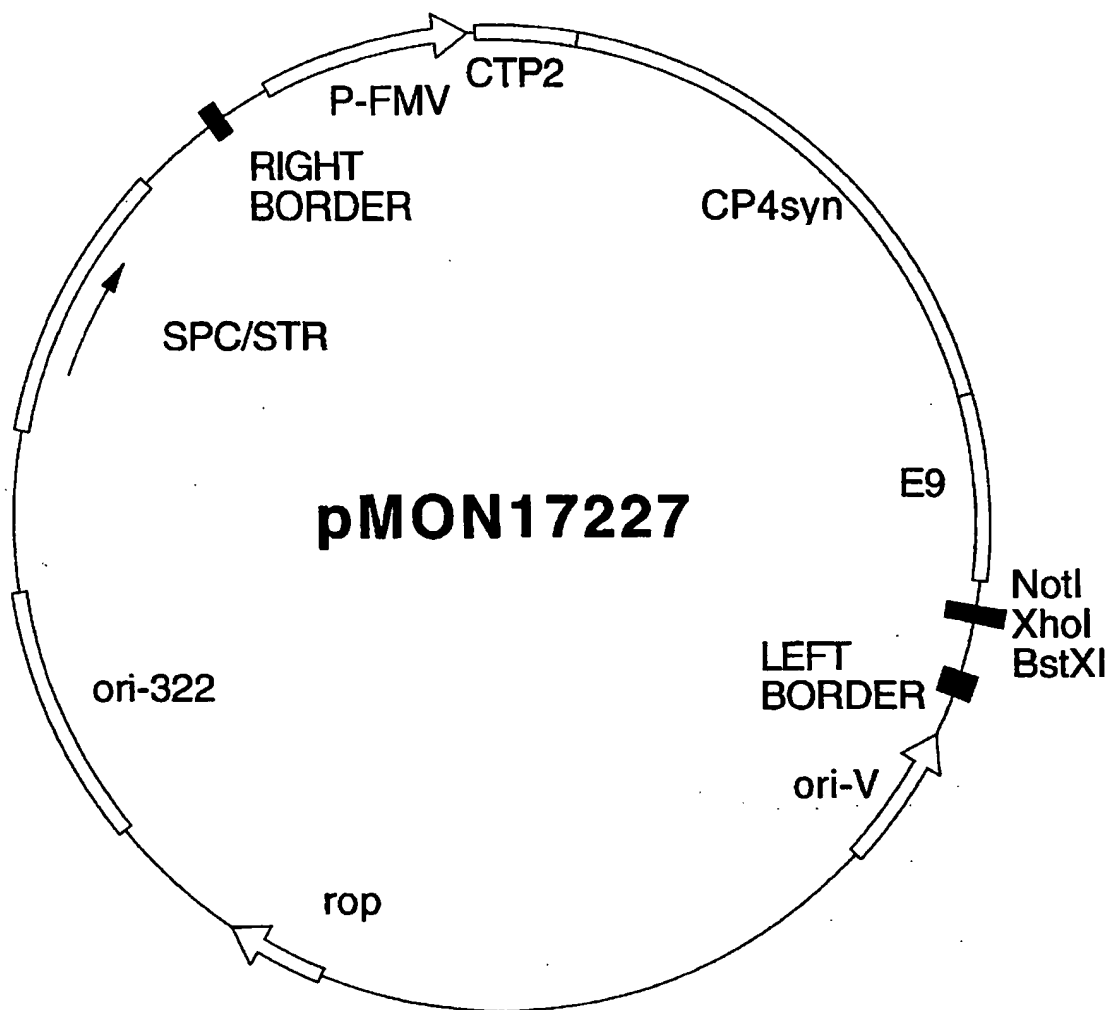
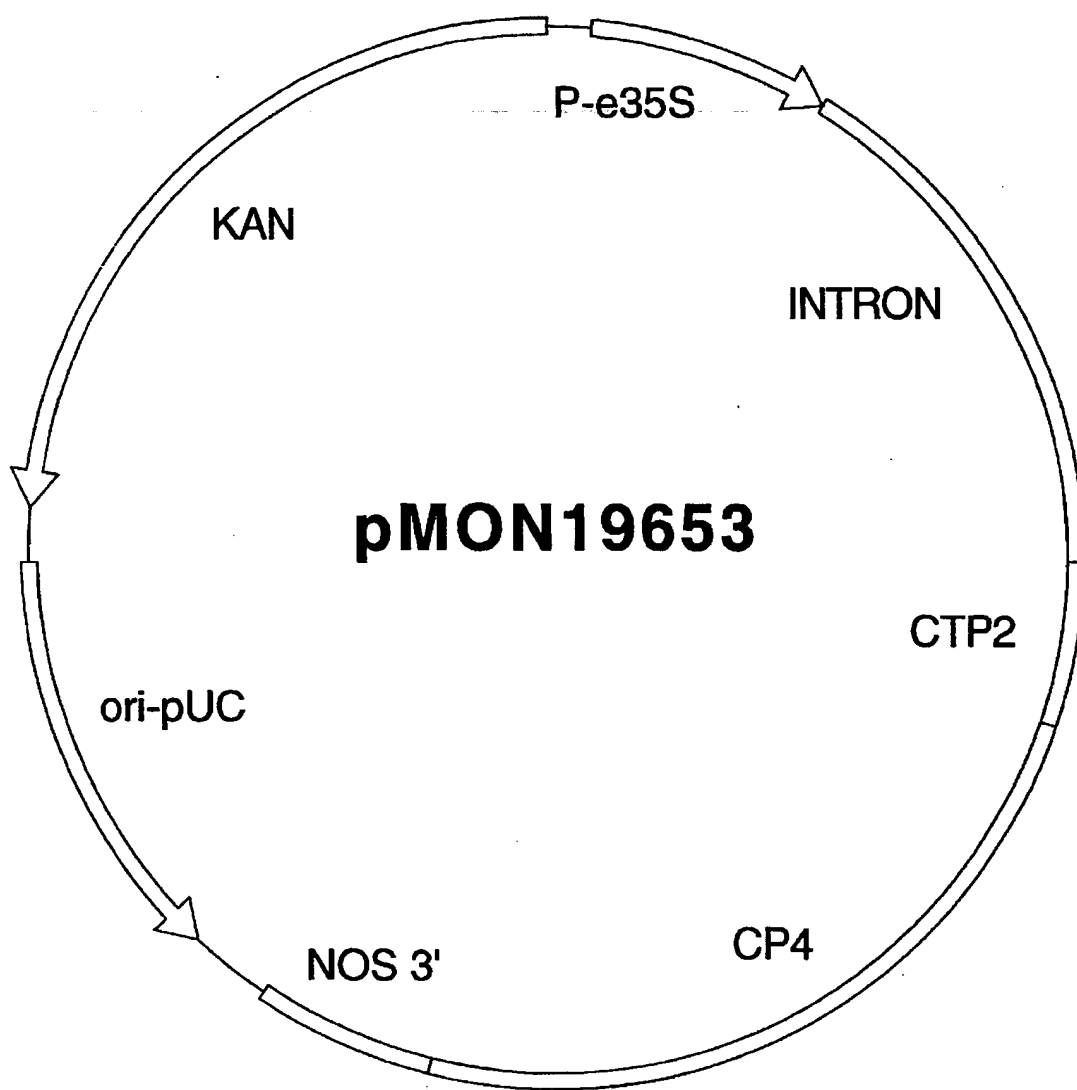


Figure 14



**Figure 15**

**Figure 16**



**Figure 17**

ATG AAA CGA GAT AAG GTG CAG ACC TTA CAT GGA GAA ATA CAT ATT CCC	48
Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro	15
1	
GGT GAT AAA TCC ATT TCT CAC CGC TCT GTT ATG TTT GGC GCG CTA GCG	96
Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala	30
20	
GCA GGC ACA ACA GTT AAA AAC TTT CTG CCG GGA GCA GAT TGT CTG	144
Ala Gly Thr Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu	45
35	
AGC ACG ATC GAT TGC TTT AGA AAA ATG GGT GTT CAC ATT GAG CAA AGC	192
Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser	60
50	
AGC AGC GAT GTC GTG ATT CAC GGA AAA GGA ATC GAT GCC CTG AAA GAG	240
Ser Ser Asp Val Val Ile Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu	80
65	
CCA GAA AGC CTT TTA GAT GTC GGA AAT TCA GGT ACA ACG ATT CGC CTG	288
Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu	95
85	
ATG CTC GGA ATA TTG GCG GGC CGT CCT TTT TAC AGC GCG GTA GCC GGA	336
Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	110
100	

Figure 18A

384 GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG  
 Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu  
 115 120 125  
 432 AAA AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGA GAG TTT ACA  
 Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Glu Phe Thr  
 130 135 140  
 480 CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA  
 Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser  
 145 150 155 160  
 528 CCT GTT GCA AGC GCG CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA TTA  
 Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Ala Gly Leu  
 165 170 175  
 576 CAG GCT GAG GGC ACA ACT GTA ACA GAG CCC CAT AAA TCT CGG GAC  
 Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp  
 180 185 190  
 624 CAC ACT GAG CGG ATG CTT TCT GCT TTT GGC GTT AAG CTT TCT GAA GAT  
 His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp  
 195 200 205  
 672 CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT  
 Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp  
 210 215 220

Figure 18B

ATT TTT GTT CCT GGA GAC ATT TCT TCA GCC GCG TTT TTC CTT GCT GCT	720
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala	240
225	
GGC GCG ATG GTT CCA AAC AGC AGA ATT GTA TTG AAA AAC GTA GGT TTA	768
Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu	255
245	
AAT CCG ACT CGG ACA GGT ATT ATT GAT GTC CTT CAA AAC ATG GGG GCA	816
Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala	270
265	
AAA CTT GAA ATC AAA CCA TCT GCT GAT AGC GGT GCA GAG CCT TAT GGA	864
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly	285
275	
GAT TTG ATT ATA GAA ACG TCA TCT CTA AAG GCA GTT GAA ATC GGA GGA	912
Asp Leu Ile Ile Glu Thr Ser Ser Ser Leu Lys Ala Val Glu Ile Gly Gly	300
290	
GAT ATC ATT CCG CGT TTA ATT GAT GAG ATC CCT ATC ATC GCG CTT CTT	960
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu	315
305	
GGC ACT CAG GCG GAA GGA ACC ACC GTT ATT AAG GAC GCG GCA GAG CTA	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	330
325	
	335

Figure 18C

AAA GTG AAA GAA ACA AAC CGT ATT GAT ACT GTT GTT TCT GAG CTT CGC	1056
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Ser Glu Leu Arg	
	340
	345
AAG CTG GGT GCT GAA ATT GAA CCG ACA GCA GAT GGA ATG AAG GTT TAT	1104
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr	
	355
	360
	365
GGC AAA CAA ACG TTG AAA GGC GGC GCT GCA GTG TCC AGC CAC GGA GAT	1152
Gly Lys Gln Thr Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp	
	370
	375
	380
CAT CGA ATC GGA ATG ATG CTT GGT ATT GCT TCC TGT ATA ACG GAG GAG	1200
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu	
	385
	390
	395
CCG ATT GAA ATC GAG CAC CAC GAT GCC ATT CAC GTT TCT TAT CCA ACC	1248
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr	
	405
	410
	415
TTC TTC GAG CAT TTA AAT AAG CTT TCG AAA AAA TCC TGA	1287
Phe Phe Glu His Leu Asn Lys Lys Ser Lys Lys Ser	
	420
	425

Figure 18D

ATG GTA AAT GAA CAA ATC ATT GAT ATT TCA GGT CCG TTA AAG GGC GAA	48
Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu	15
1	
5	
10	
ATA GAA GTG CCG GGC GAT AAG TCA ATG ACA CAC CGT GCA ATC ATG TTG	96
Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	30
20	
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920	
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955	
960	
965	
970	
975	
980	
985	
990	
995	
1000	

Figure 19A



TTG TCT GGC GAT GTT TCA ATT GGT AAA AGG CCA ATG GAT CGT GTC TTG	384
Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu	
	115
	120
	125
AGA CCA TTG AAA CTT ATG GAT GCG AAT ATT GAA GGT ATT GAA GAT AAT	432
Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn	
	130
	135
	140
TAT ACA CCA TTA ATT ATT AAG CCA TCT GTC ATA AAA GGT ATA AAT TAT	480
Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr	
	145
	150
	155
CAA ATG GAA GTT GCA AGT GCA CAA GTA AAA AGT GCC ATT TTA TTT GCA	528
Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala	
	165
	170
	175
AGT TTG TTT TCT AAG GAA CCG ACC ATC ATT AAA GAA TTA GAT GTA AGT	576
Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser	
	180
	185
	190
CGA AAT CAT ACT GAG ACG ATG TTC AAA CAT TTT AAT ATT CCA ATT GAA	624
Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu	
	195
	200
	205
GCA GAA GGG TTA TCA ATT AAT ACA ACC CCT GAA GCA ATT CGA TAC ATT	672
Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile	
	210
	215
	220

Figure 19B

720  
 AAA CCT GCA GAT TTT CAT GTT CCT GGC GAT ATT TCA TCT GCA GCG TTC  
 Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe  
 225 230 235 240  
 768  
 TTT ATT GTT GCA GCA CTT ATC ACA CCA GGA AGT GAT GTA ACA ATT CAT  
 phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His  
 245 250 255  
 816  
 AAT GTT GGA ATC AAT CAA ACA CGT TCA GGT ATT ATT GAT ATT GTT GAA  
 Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu  
 260 265 270  
 864  
 AAA ATG GGC GGT AAT ATC CAA CTT TTC AAT CAA ACA ACT GGT GCT GAA  
 Lys Met Gly Gly Asn Ile Gln Leu Phe Phe Asn Gln Thr Thr Gly Ala Glu  
 275 280 285  
 912  
 CCT ACT GCT TCT ATT CGT ATT CAA TAC ACA CCA ATG CTT CAA CCA ATA  
 Pro Thr Ala Ser Ile Arg Ile Gln Thr Tyr Thr Pro Met Leu Gln Pro Ile  
 290 295 300  
 960  
 ACA ATC GAA GGA GAA TTA GTT CCA AAA GCA ATT GAT GAA CTG CCT GTA  
 Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val  
 305 310 315 320  
 1008  
 ATA GCA TTA CTT TGT ACA CAA GCA GTT GGC ACG AGT ACA ATT AAA GAT  
 Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp  
 325 330 335

Figure 19C

GCC GAG GAA TTA AAA GTA AAA GAA ACA AAT AGA ATT GAT ACA ACG GCT Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala 340 345 350	1056
GAT ATG TTA AAC TTG TTA TTA GGG TTT GAA TTA CAA CCA ACT AAT GAT GGA Asp Met Leu Asn Leu Leu Leu Phe Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly 355 360 365	1104
TTG ATT ATT CAT CCG TCA GAA TTT AAA ACA AAT GCA ACA GAT ATT TTA Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu 370 375 380	1152
ACT GAT CAT CGA ATA GGA ATG ATG CTT GCA GTT GCT TGT GTA CTT TCA Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser 385 390 395	1200
AGC GAG CCT GTC AAA ATC AAA CAA TTT GAT GCT GTA AAT GTA TCA TTT Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe 400 405 410 415	1248
CCA GGA TTT TTA CCA AAA CTA AAG CTT TTA CAA AAT GAG GGA TAA Pro Gly Phe Leu Pro Lys Leu Lys Lys Leu Leu Gln Asn Glu Gly 420 425 430	1293

Figure 19D

1	PG2982	.....	.....	.....	.....	MSHSASPKPA	TARRSEALTG	50
	LBAA	.....	.....	.....	.....	MSHSASPKPA	TARRSEALTG	
	Agrobacterium CP4	.....	.....	.....	.....	MSHGASSRPA	TARKSSGLSG	
	B. subtilis	.....	.....	.....	.....	.....M	KRDKVQTLHG	
	S. aureus	.....	.....	.....	.....	MVNEQ	IIDISGPLKG	
	S. cerevisiae	.....	.....	.....	.....	LVYP	FKDIPADQOK	
	A. nidulans	.....	.....	.....	.....	.....VHP	..GVAHSSNV	
	B. napus	.....	.....	.....	.....	K...ASEI	VLQPIREISG	
	A. thaliana	.....	.....	.....	.....	K...ASEI	VLQPIREISG	
	N. tabacum	.....	.....	.....	.....	K...PNEI	VLQPIKDISG	
	L. esculentum	.....	.....	.....	.....	K...PHEI	VLXPIKDISG	
	P. hybrida	.....	.....	.....	.....	K...PSEI	VLQPIKEISG	
	Z. mays	.....	.....	.....	.....	AGAEI	VLQPIKEISG	
	S. gallinarum	.....	.....	.....	.....	.....MESL	TLQPIARVDG	
	S. typhimurium	.....	.....	.....	.....	.....MESL	TLQPIARVDG	
	S. typhi	.....	.....	.....	.....	.....MESL	TLQPIARVDG	
	E. coli	.....	.....	.....	.....	.....MESL	TLQPIARVDG	
	K. pneumoniae	.....	.....	.....	.....	.....MESL	TLQPIARVDG	
	Y. enterocolitica	.....	.....	.....	.....	.....MLESL	TLHPIALING	
	H. influenzae	.....	.....	.....	.....	.....MEKI	TLAPISAVEG	
	P. multocida	.....	.....	.....	.....	..MIKDATAI	TLNPISYIEG	
	A. salmonicida	.....	.....	.....	.....	.....NSL	RLEPISRVAG	
	B. pertussis	.....	.....	.....	.....	..MSGLAYL	DLPAARLARG	
	Consensus	-----	-----	-----	-----	-----	-----	

Figure 20A

51	PG2982	100
	LBAA	
Agrobacterium CP4	EIRIPGDKSI	SHRSMFEGGL ASGETRITGL LEGEDVINTG RAMQAM.GAK
B. subtilis	EIRIPGDKSI	SHRSMFEGGL ASGETRITGL LEGEDVINTG RAMQAM.GAK
S. aureus	TVRIPGDKSI	SHRSMFEGGL ASGETRITGL LEGEDVINTG KAMQAM.GAR
	EIHIPGDKSI	SHRSMFEGAL AAGTTTVKNF LPGADCLSTI DCFRKM.GVH
	EIEVPGDKSM	THRAIMLASL AEGVSTIYKP LLGEDCRRTM DIFRHL.GVE
S. cerevisiae	VVIPGSKSI	SNRALLAAL GEGQCKIKNL LHSDDTKHML TAVHELKAT
A. nidulans	ICAPPGSKSI	SNRALVLAAL GSGTCRIKNL LHSDDTVVML NALERLGAAT
B. napus	LIKLPGSKSL	SNRIILLAAL SEGTTVVDNL LNSDDINYML DALKKL.GLN
A. thaliana	LIKLPGSKSL	SNRIILLAAL SEGTTVVDNL LNSDDINYML DALKRL.GLN
N. tabacum	TVKLPGSKSL	SNRIILLAAL SKGRTVVDNL LSSDDIHYML GALKTL.GLH
L. esculentum	TVKLPGSKSL	SNRIILLAAL SEGRVVDNL LSSDDIHYML GALKTL.GLH
P. hybrida	TVKLPGSKSL	SNRIILLAAL SEGTTVVDNL LSSDDIHYML GALKTL.GLH
Z. mays	TVKLPGSKSL	SNRIILLAAL SEGTTVVDNL LNSEDVHYML GALRTL.GLS
S. gallinarum	AINLPGSKSV	SNRALLAAL ACCKTVLTNL LDSDDVRHML NALSAL.GIN
S. typhimurium	AINLPGSKSV	SNRALLAAL PCGKTALTNL LDSDDVRHML NALSAL.GIN
S. typhi	AINLPGSKSV	SNRALLAAL ACCKTVLTNL LDSDDVRHML NALSAL.GIN
E. coli	TINLPGSKTV	SNRALLAAL AHGKTVLTNL LDSDDVRHML NALTAL.GVS
K. pneumoniae	TVNLPGSKSV	SNRALLAAL ARGTTVLTNL LDSDDVRHML NALSAL.GVH
Y. enterocolitica	TVNLPGSKSV	SNRALLAAL AEGTTQLNNL LDSDDIRHML NALQAL.GVK
H. influenzae	TINLPGSKSL	SNRALLAAL AKGTTKVTNL LDSDDIRHML NALKAL.GVR
P. multocida	EVRLPGSKSL	SNRALLLSAL AKGTTTLTNL LDSDDVRHML NALKEL.GVT
A. salmonicida	EVNLPGSKSV	SNRALLAAL ARGTTTLTNL LDSDDIRHML AALTQL.GVK
B. pertussis	EVALPGSKSI	SNRVLLAAL AEGSTEITGL LDSDDTRVML AALRQL.GVS
Consensus	----PG-K-- --R-----L --G-----L-----D-----	

Figure 20B

PG2982	101	IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY	150
LBAA		IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY	
Agrobacterium CP4		IRKEGDTWII	DGVNGGGLLA	P.....EAP	LDFGNAATGC	RLTMGLVGTV	
B. subtilis		IEQSSSDVVI	HGKGIDALKE	P.....ESL	LDVNSGTTI	RLMLGILAGR	
S. aureus		IKEDDEKLIV	TSPGYQ.VNT	P.....HQV	LYTNSGTTT	RLLAGLLSGL	
S. cerevisiae		ISWEDNGETV	VVEGHGG...	.STLSACADP	LYLGNAGTAS	RFLTSLAALV	
A. nidulans		FSWEEEGEVL	VVNGKGG...	..NLQASSP	LYLGNAGTAS	RFLTTVATLA	
B. napus		VERDSVNNRA	VVEGCGGIFP	ASLDSKSDIE	LYLGNAGTAM	RPLTAAAVTAA	
A. thaliana		VETDSENNRA	VVEGCGGIFP	ASIDSKSDIE	LYLGNAGTAM	RPLTAAAVTAA	
N. tabacum		VEDDNNENQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAAVTVA	
L. esculentum		VEDDNNENQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAAVTVA	
P. hybrida		VEEDSANQRA	VVEGCGGLFP	VGKESKEEIQ	LFLGNAGTAM	RPLTAAAVTVA	
Z. mays		VEADKAAKRA	VVVGCGGKFP	VE.DAKEEVQ	LFLGNAGTAM	RPLTAAAVTAA	
S. gallinarum		YTLSADRTRC	DITNGGGPLR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhimurium		YTLSADRTRC	DITNGGGALR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhi		YTLSADRTRC	DITNGGGPLR	AS....GTLE	LFLGNAGTAM	RPLAAALCL.	
E. coli		YTLSADRTRC	EIIGNGGPLH	AE....GALE	LFLGNAGTAM	RPLAAALCL.	
K. pneumoniae		YVLSSDRTRC	EVTGTGGPLQ	AG....SALE	LFLGNAGTAM	RPLAAALCL.	
Y. enterocolitica		YRLSADRTRC	EVDGLGKLV	AE....QPLE	LFLGNAGTAM	RPLAAALCL.	
H. influenzae		YQLSDDKTIC	EIEGLGAFN	IQ....DNLS	LFLGNAGTAM	RPLTAAALCLK	
P. multocida		YQLSEDKSVC	EIEGLGRAFE	WQ....SGLA	LFLGNAGTAM	RPLTAAALCLS	
A. salmonicida		YKLSADKTEC	TVHGLGRSFA	VS....APVN	LFLGNAGTAM	RPLCAALCL.	
B. pertussis		VGEVAD..GC	VTIEGVARFP	TE.....QAE	LFLGNAGTAF	RPLTAAALAM	
Consensus		-----	-----	-----	L--GN--T--	R-----	

Figure 20C

PG2982	151	DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	200
LBAA		DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	
Agrobacterium CP4		DF.....DS	TFIGDASLTK	RPMGRVLNPL	REMGVQVKSE	DGDRLPVT..	
B. subtilis		PF.....YS	AVAGDESIK	RPMKRVTEPL	KKMGAKIDGR	AGGEFTPL..	
S. aureus		GN.....ES	VLSGDVSIGK	RPMDRVLRPL	KLMDANIEG.	IEDNYTPL..	
S. cerevisiae		NST.SSQYI	VLGTGNARMQ	RPIAPLVDSL	RANGTKIEYL	NNEGSLPIKV	
A. nidulans		NS...STVDSS	VLGTGNRMKQ	RPIGDLVDAL	TANVLPLNTS	KGRASLPLKI	
B. napus		G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTNCPVVRV	
A. thaliana		G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTNCPVVRV	
N. tabacum		G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTNCPVRI	
L. esculentum		G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCS	LGTNCPVRI	
P. hybrida		G....GNSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTNCPVRI	
Z. mays		G....GNATY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVDCF	LGTDCPPVRV	
S. gallinarum		....GQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPRLRL	
S. typhimurium		....GQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPRLRL	
S. typhi		....GQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPRLRL	
E. coli		....GSNDI	VLTEPRMKE	RPIGHLVDAL	RLGGAKITYL	EQENYPPRLRL	
K. pneumoniae		....GSNDI	VLTEPRMKE	RPIGHLVDAL	RQGGAQIDYL	EQENYPPRLRL	
Y. enterocolitica		....GKNDI	VLTEPRMKE	RPIGHLVDAL	RQGGAQIDYL	EQENYRR.CI	
H. influenzae		G.NHEV..EI	ILTGEPRMKE	RPILHLVDAL	RQAGADIRYL	ENEGYPPPLAI	
P. multocida		TPNREGKNEI	VLTEPRMKE	RPIQHLVDAL	CQAGAEIQYL	EQEGYPPPIAI	
A. salmonicida		....GSGEY	MLGGEPRMEE	RPIGHLVDCL	ALKGAGHIQYL	KKDGYPPPLV	
B. pertussis		G.....GDY	RLSGVPRMHE	RPIGDLVDAL	RQFGAGIEYL	GQAGYPPPLRI	
Consensus		-----G-----	RP-----L	-----	-----	-----	

Figure 20D

PG2982	201	LIGPK	TANPITYRVP	MASQVKS	AV	LLAGLN	250	TPGVTT
LBAA		LIGPK	TANPITYRVP	MASQVKS	AV	LLAGLN		TPGVTT
Agrobacterium CP4		LRGPK	TPPITYRVP	MASQVKS	AV	LLAGLN		TPGITT
B. subtilis		SVSGA	SLKGIDYVSP	VASQIKS	AV	LLAGLQ		AEGTTT
S. aureus		IIKPS	VIKGINYQME	VASQVKS	AI	LFASLF		SKEPTI
S. cerevisiae		YTDSVFKG	..	GRIELAA	TVSSQYVSSI	LMCAPYAE		EPVTLALVG
A. nidulans		AASGGFAG	..	GNINLAA	KVSSQYVSSL	LMCAPYAK		EPVTLRLVG
B. napus		NANGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
A. thaliana		NANGGLPG	..	GKVKLSG	SISSQYLTL	LMSAP.LA		LGDVEIEIV
N. tabacum		VSKGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
L. esculentum		VSKGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
P. hybrida		VSKGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
Z. mays		NGIGGLPG	..	GKVKLSG	SISSQYLSAL	LMAAP.LP		LGDVEIEII
S. gallinarum		RG..GFIG	..	GDIKVDG	SVSSQFLTL	LMTAP.LA		PKDTIIRVK
S. typhimurium		RG..GFTG	..	GDIKVDG	SVSSQFLTL	LMTAP.LA		PKDTIIRVK
S. typhi		RG..GFIG	..	GDIKVDG	SVSSQFLTL	LMTAP.LA		PEDTIIIRVK
E. coli		QG..GFTG	..	GNVDVDG	SVSSQFLTL	LMTAP.LA		PEDTIIIRVK
K. pneumoniae		RG..GFTG	..	GDVEVDG	SVSSQFLTL	LMAAP.LA		PQDTVIAIK
Y. enterocolitica		AG..GFRG	..	GKLTVDG	SVSSQFLTL	LMTAP.LA		EQDTEIQIQ
H. influenzae		RNK.GIKG	..	GKVKIDG	SISSQFLTL	LMSAP.LA		ENDTEIEII
P. multocida		RNT.GLKG	..	GRIQIDG	SVSSQFLTL	LMAAP.MA		EADTEIEII
A. salmonicida		DAK.GLWG	..	GDVHVDG	SVSSQFLTAF	LMAAPAMA		PVIPRIHIK
B. pertussis		GGGSIRVD	..	GPVRVEG	SVSSQFLTL	LMAAPVLARR		SGQDITIEV
Consensus		-----	-----	-----	-----S-Q-----	-----L-----		-----

Figure 20E



PG2982	251	VIEPVMTRDH	TEKMLQGFGA	DLTVETDKDG	VRHIRTGGQ	KLVGQ.TIDV	300
LBAA		VIEPVMTRDH	TEKMLQGFGA	DLTVETDKDG	VRHIRTGGQ	KLVGQ.TIDV	
Agrobacterium CP4		VIEPIMTRDH	TEKMLQGFGA	NLTVETDADG	VRTIRLEGRG	KLTGQ.VIDV	
B. subtilis		VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	...VSIAGGQ	KLTA.A.DIFV	
S. aureus		IKELDVSRNH	TETMFKHFN	PIEAEGLS..	..INTTPEAI	RYIKPADDFHV	
S. cerevisiae		GKPISKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI	
A. nidulans		GKPISQPYID	MTTAMMRSFG	ID..VQSTT	EEHTYHIPQG	RYVNPAEYVI	
B. napus		DKLISVPYVE	MTLKLMEFRG	VS..AEHSDS	WDRFFVKGQ	KYKSPGNAYV	
A. thaliana		DKLISVPYVE	MTLKLMEFRG	VS..VEHSDS	WDRFFVKGQ	KYKSPGNAYV	
N. tabacum		DKLISVPYVE	MTLKLMEFRG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV	
L. esculentum		DKLISVPYVE	MTLKLMEFRG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKAFV	
P. hybrida		DKLISVPYVE	MTLKLMEFRG	IS..VEHSSS	WDRFFVVRGGQ	KYKSPGKAFV	
Z. mays		DKLISIPYVE	MTLRLMEFRG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV	
S. gallinarum		GELVSKPYID	ITLNLMKTFG	VE..IAN.HH	YQFVVKGGQ	QYHSPGRYLV	
S. typhimurium		GELVSKPYID	ITLNLMKTFG	VE..IAN.HH	YQFVVKGGQ	QYHSPGRYLV	
S. typhi		GELVSKPYID	ITLNLMKTFG	VE..IAN.HH	YQFVVKGGQ	QYHSPGRYLV	
E. coli		GDLVSKPYID	ITLNLMKTFG	VE..IEN.QH	YQFVVKGGQ	SYQSPGTLYV	
K. pneumoniae		GELVSRPYID	ITLHLMKTFG	VE..VEN.QA	YQRFIVRGNG	QYQSPGDYLV	
Y. enterocolitica		GELVSKPYID	ITLHLMKAFG	VD..VVH.EN	YQIFHIKGGQ	TYRSPGIYLV	
H. influenzae		GELVSKPYID	ITLAMMRDFG	VK..VEN.HH	YQKFQVKGNQ	SYISPNKYLV	
P. multocida		GELVSKPYID	ITLKMMQTFG	VE..VEN.QA	YQRFVVKGHQ	QYQSPHRFLV	
A. salmonicida		GELVSKPYID	ITLHIMNSSG	VV..IEH.DN	YKLFYIKGNQ	SIVSPGDFLV	
B. pertussis		GELISKPYIE	ITLNLMARFG	VS..V.RRDG	WRAFTIARDA	VYRGPGRMAI	
Consensus		-----	-----	-----	-----	-----	

Figure 20F

PG2982	PGDPSSTAFF	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	350
LBAA	PGDPSSTAFF	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	
Agrobacterium CP4	PGDPSSTAFF	LVAALLVPGS	DVTILNVLMN	PTRTGL...	I	LTLQEMGADI	
B. subtilis	PGDISSAAFF	LAAGAMVPNS	RIVLKNVGLN	PTRTGI...	I	DVLQNMGA KL	
S. aureus	PGDISSAAFF	IVAALITPGS	DVTIHNVGIN	QTRSGI...	I	DIVEKMGGNI	
S. cerevisiae	ESDASSATYP	LAFAA.MTGT	TVTVPNIGFE	SLQGDARFAR		DVLKPMGCKI	
A. nidulans	ESDASSATYP	LAVAA.VTGT	TCTVPNIGSA	SLQGDARFAV		EVLRPMGCTV	
B. napus	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLQGDVKFA.		EVLEKMGCKV	
A. thaliana	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLQGDVKFA.		EVLEKMGCKV	
N. tabacum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLQGDVKFA.		EVLEKMGAEV	
L. esculentum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLQGDVKFA.		EVLEKMGAEV	
P. hybrida	EGDASSASYF	LAGAA.VTGG	TITVEGCGTN	SLQGDVKFA.		EVLEKMGAEV	
Z. mays	EGDASSASYF	LAGAA.ITGG	TVTVEGCGTT	SLQGDVKFA.		EVLEMMGAKV	
S. gallinarum	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhimurium	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhi	EGDASSASYF	LAAGG.IKGG	TVKVTGIGGK	SMQGDIRFA.		DVLHKMGATI	
E. coli	EGDASSASYF	LAAA.IKGG	TVKVTGIGRN	SMQGDIRFA.		DVLEKMGATI	
K. pneumoniae	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRN	SVQGDIRFA.		DVLEKMGATV	
Y. enterocolitica	EGDASSASYF	LAAA.IKGG	TVRVTGIGKQ	SVQGDTKFA.		DVLEKMGAKI	
H. influenzae	EGDASSASYF	LAAGA.IK.G	KVKVTGIGKN	SIQGDRLFA.		DVLEKMGAKI	
P. multocida	EGDASSASYF	LAAA.IK.G	KVKVTGVGKN	SIQGDRLFA.		DVLEKMGAKI	
A. salmonicida	EGDASSASYF	LAAGA.IK.G	KVRVTGIGKH	SI.GDIHFA.		DVLERMGARI	
B. pertussis	EGDASTASYF	LALGA.IGGG	PVRVTGVGED	SIQGDVAFA.		ATLAAMGADV	
Consensus	--D-S----	-----	-----	-----		-----MG----	

Figure 20G

351	PG2982	351	EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE	400	YPVLAIAASF
	LBAA		EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE		YPVLAIAASF
	Agrobacterium CP4		EDVADLRVR.	SSTLKGVTVP	EDRAPSMIDE		YPILAVAAAF
	B. subtilis		EPYGDLLIE.	TSSLKAVEIG	GDIIPRLIDE		IPIIALLATQ
	S. aureus		EPTASIRIQY	TPMLQIPITIE	GELVPKAIDE		LPVIALLCCTQ
	S. cerevisiae		TTVSGPPV..	...GTLKPLK	HVDMPEMTDA		FLTACVVAAI
	A. nidulans		TTVTGPSD..	...GILRATS	KRGYGT.NDR		CVPRCFTGS
	B. napus		VTVTGPSRDA	FGMRHLRAV.	DVNMNKMPPDV		AMTLAVVALF
	A. thaliana		VTVTGPPrDA	FGMRHLRAI.	DVNMNKMPPDV		AMTLAVVALF
	N. tabacum		VTVKGPPRNS	SGMKHLRAV.	DVNMNKMPPDV		AMTLAVVALF
	L. esculentum		VTVKGPPRNS	SGMKHLRAI.	DVNMNKMPPDV		AMTLAVVALF
	P. hybrida		VTVKGPPRSS	SGRKHLRAI.	DVNMNKMPPDV		AMTLAVVALY
	Z. mays		VTVTGPPrEP	FGRKHLKAI.	DVNMNKMPPDV		AMTLAVVALF
	S. gallinarum		I.....A	CTRGELHAI.	DMDMNHIPDA		AMTIATTALF
	S. typhimurium		I.....A	CTRGELHAI.	DMDMNHIPDA		AMTIATTALF
	S. typhi		I.....A	CTRGELHAI.	DMDMNHIPDA		AMTIATTALF
	E. coli		I.....S	CTRGELNAI.	DMDMNHIPDA		AMTIATAALF
	K. pneumoniae		I.....A	CTRGELNAI.	DMDMNHIPDA		AMTIATAALF
	Y. enterocolitica		I.....E	CSRGELQGI.	DMDMNHIPDA		AMTIATTALF
	H. influenzae		I.....Q	AEHAELNGI.	DMDMNHIPDA		AMTIATTALF
	P. multocida		I.....Q	VEKGNLKGI.	DMDMNHIPDA		AMTIATTALF
	A. salmonicida		I.....E	AEQGPHGV.	DMDMNHIPDV		GHDHSGQSHC
	B. pertussis		IETRGVRAE	GGR..LKAF.	DADFNLIPIA		AMTAATLALY
	Consensus		-----D-----	-----D-----			-----D-----

Figure 20H

PG2982	401	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV	450	DCTEGEMSLT
LBAA	AEG.....	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV		DCTEGEMSLT
Agrobacterium CP4	AEG.....	ATVMNGLEEL	RVKESDRLSA	VANGLKLVG		DCDEGETSLV
B. subtilis	AEG.....	TTVIKDAEEL	KVKETNRIDT	VVSELRLKGA		EIEPTADGMK
S. aureus	AVG.....	TSTIKDAEEL	KVKETNRIDT	TADMLNLLGF		ELQPTNDGLI
S. cerevisiae	SHSDPNNSAN	TTTIEGIANQ	RVKECNRLA	MATELAKFGV		KTTELPDGIQ
A. nidulans	HRPMEKSQTT	PPVSSGIANQ	RVKECNRIKA	MKDELAKEFGV		ICREHDDGLE
B. napus	ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV.EEGSDYC
A. thaliana	ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV.EEGSDYC
N. tabacum	ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA		TV.VEGSDYC
L. esculentum	ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV.VEGSDYC
P. hybrida	ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA		TV.EEGPDYC
Z. mays	ADG.....	PTAIRDVASW	RVKETERMVA	IRTELTKLGA		SV.EEGPDYC
S. gallinarum	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
S. typhimurium	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
S. typhi	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
E. coli	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
K. pneumoniae	ARG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGEDI
Y. enterocolitica	ADG.....	PTVIRNIYNW	RVKETDRLSA	MATELRKVGA		EV.EEGQDI
H. influenzae	SNG.....	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA		EV.EEGEDFI
P. multocida	AEG.....	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA		EV.EEGEDFI
A. salmonicida	LPR.....	VPPHSQHLQL	AVRD.DRCTP	CTHGHRRQA		GVSEEGTTFI
B. pertussis	ADG.....	PCRLRNIGSW	RVKETDRIHA	MHTELEKLGA		GV.QSGADWL
Consensus	-----	-----	-V-----R-	-----		-----

Figure 20I

PG2982	451	VRGRPDGKGL	G...GG....	TVATHLDHRI	AMSFLVMGLA	500
LBAA		VRGRPDGKGL	G...GG....	TVATHLDHRI	AMSFLVMGLA	.....A
Agrobacterium CP4		VRGRPDGKGL	GNASGA....	AVATHLDHRI	AMSFLVMGLV	.....S
B. subtilis		VYGKQTLKG.	....GA....	AVSSHGDHRI	GMMLGIASCI	.....T
S. aureus		IHPSEFKTN.	....AT....	DI..LTDHRI	GMMLAVACVL	.....S
S. cerevisiae		VHGLNSIKDL	KVPSDSSGPV	GVCTYDDHRV	AMSFSLLAGM	VNSQNERDEV
A. nidulans		IDGIDR.SNL	RQPVG....	GVFCYDDHRV	AFSFSVL.SL	VTPQ.....
B. napus		VITP..PAKV	KPA.....	EIDTYDDHRM	AMAFSLAAC.	.....A
A. thaliana		VITP..PKKV	KTA.....	EIDTYDDHRM	AMAFSLAAC.	.....A
N. tabacum		IITP..PEKL	NVT.....	EIDTYDDHRM	AMAFSLAAC.	.....A
L. esculentum		IITP..PEKL	NVT.....	EIDTYDDHRM	AMAFSLAAC.	.....A
P. hybrida		IITP..PEKL	NVT.....	DIDTYDDHRM	AMAFSLAAC.	.....A
Z. mays		IITP..PEKL	NVT.....	AIDTYDDHRM	AMAFSLAAC.	.....A
S. gallinarum		RITP..PAKL	QHA.....	DIGTYNDHRM	AMCFSLVAL.	.....S
S. typhimurium		RITP..PAKL	QHA.....	DIGTYNDHRM	AMCFSLVAL.	.....S
S. typhi		RITP..PAKL	QHA.....	DIGTYNDHRM	AMCFSLVAL.	.....S
E. coli		RITP..PEKL	NFA.....	EIATYNDHRM	AMCFSLVAL.	.....S
K. pneumoniae		RITP..PLTL	QFA.....	EIGTYNDHRM	AMCFSLVAL.	.....S
Y. enterocolitica		RVVP..PAQL	IAA.....	EIGTYNDHRM	AMCFSLVAL.	.....S
H. influenzae		RIQPLALNQF	KHA.....	NIETYNDRM	AMCFSLIAL.	.....S
P. multocida		RIQPLNLAQF	QHA.....	ELNI.HDHRM	AMCFALIAL.	.....S
A. salmonicida		TRDAADPAQA	RRD.....	R..HLQRSRI	AMCFSLVAL.	.....S
B. pertussis		EVAPPEPGGW	RDA.....	HIGTWDDHRM	AMCFLLAFF.	.....G
Consensus		-----	-----	-----R-	-----	-----

Figure 20J

501	PG2982	EKPVTVDSDN	MIATSFPEFM	DMMPGLGAKI	ELSIL...	538
	LBAA	EKPVTVDSDN	MIATSFPEFM	DMMPGLGAKI	ELSIL...	
	Agrobacterium CP4	ENPVTVDSDAT	MIATSFPEFM	DLMAGLGAKI	ELSDTKAA	
	B. subtilis	EEPIEIEHTD	AIHVSYPTEF	EHLNKLKSKS	.....	
	S. aureus	SEPVKIKQFD	AVNVSFPGFL	PKLKLQNEG	.....	
	S. cerevisiae	ANPVRILERH	CTGKTWPGWW	DVLH.....	.....	
	A. nidulans	..PTLILEKE	CVGKTWPGWW	DTLRQLFKV.	.....	
	B. napus	DVPVTIKDPG	CTRKTFFPDYF	QVLESITKH.	.....	
	A. thaliana	DVPITINDSG	CTRKTFFPDYF	QVLERITKH.	.....	
	N. tabacum	DVPVTIKDPG	CTRKTFFPNYF	DVLQQYSKH.	.....	
	L. esculentum	DVPVTIKNPG	CTRKTFFPDYF	EVLQKYSKH.	.....	
	P. hybrida	DVPVTINDPG	CTRKTFFPNYF	DVLQQYSKH.	.....	
	Z. mays	EVPVTIRDPG	CTRKTFFPDYF	DVLSTFVKN.	.....	
	S. gallinarum	DTPVTILDPK	CTAKTFFPDYF	EQLARMSTPA	.....	
	S. typhimurium	DTPVTILDPK	CTAKTFFPDYF	EQLARMSTPA	.....	
	S. typhi	DTPVTILDPK	CTAKTFFPDYF	EQLARMSTPA	.....	
	E. coli	DTPVTILDPK	CTAKTFFPDYF	EQLARISQAA	.....	
	K. pneumoniae	DTPVTILDPK	CTAKTFFPDYF	GQLARISTLA	.....	
	Y. enterocolitica	DTPVTILDPK	CTAKTFFPDYF	EQLARLSQIA	.....	
	H. influenzae	NTPVTILDPK	CTAKTFFTEFF	NEFE....KI	CLKN.....	
	P. multocida	KTSVTILDPS	CTAKTFFTEFF	ILFTLNTREV	AYR.....	
	A. salmonicida	DIAVTINDPG	CTSKTFFPDYF	DKLASVSQAV	.....	
	B. pertussis	PAAVRILDPG	CVSKTFFPDYF	DVYAGLLAAR	D.....	
	Consensus	-----P-----	-----P-----	-----P-----	-----P-----	

Figure 20K

ACGGGCTGTA ACGGTAGTAG GGGTCCCAG CACAAAAGCG GTGCCGGCAA GCAGAACTAA 60  
TTTCCATGGG GAATAATGGT ATTTTCATGG TTTGGCCTCT GGTCTGGCAA TGGTTGCTAG 120  
GCGATCGCCT GTTGAAATTA ACAAACTGTC GCCCTTCCAC TGACCATGGT AACGATGTTT 180  
TTTACTTTCCT TGACTAACCG AGGAAAATTT GGCGGGGGGC AGAAATGCCA ATACAATTTA 240  
GCTTGGTCTT CCCTGCCCCCT AATTGTCCC CTCC ATG GCC TTG CTT TCC CTC 292  
Met Ala Leu Leu Ser Leu  
1 5  
AAC AAT CAT CAA TCC CAT CAA CGC TTA ACT GTT AAT CCC CCT GCC CAA 340  
Asn Asn His Gln Ser His Gln Arg Leu Thr Val Asn Pro Pro Ala Gln  
10 15 20  
GGG GTC GCT TTG ACT GGC CGC CTA AGG GTG CCG GGG GAT AAA TCC ATT 388  
Gly Val Ala Leu Thr Gly Arg Leu Arg Val Pro Gly Asp Lys Ser Ile  
25 30 35  
TCC CAT CGG GCC TTG ATG TTG GGG GCG ATC GCC ACC GGG GAA ACC ATT 436  
Ser His Arg Ala Leu Met Leu Gly Ala Ile Ala Thr Gly Glu Thr Ile  
40 45 50  
ATC GAA GGG CTA CTG TTG GGG GAA GAT CCC CGT AGT ACG GCC CAT TGC 484  
Ile Glu Gly Leu Leu Leu Gly Glu Asp Pro Arg Ser Thr Ala His Cys  
55 60 65 70

Figure 21A

532 TTT CGG GCC ATG GGA GCA GAA ATC AGC GAA CTA AAT TCA GAA AAA ATC  
 Phe Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile  
 75 80 85  
 580 ATC GTT CAG GGT CGG GGT CTG GGA CAG TTG CAG GAA CCC AGT ACC GTT  
 Ile Val Gln Gly Arg Gly Leu Gly Gln Leu Glu Pro Ser Thr Val  
 90 95 100  
 628 TTG GAT GCG GGG AAC TCT GGC ACC ACC ATG CGC TTA ATG TTG GGC TTG  
 Leu Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu  
 105 110 115  
 676 CTA GCC GGG CAA AAA GAT TGT TTA TTC ACC GTC ACC GGC GAT GAT TCC  
 Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr Thr Val Thr Gly Asp Ser  
 120 125 130  
 724 CTC CGT CAC CGC CCC ATG TCC CGG GTA ATT CAA CCC TTG CAA CAA ATG  
 Leu Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met  
 135 140 145  
 772 GGG GCA AAA ATT TGG GCC CGG AGT AAC GGC AAG TTT GCG CCG CTG GCA  
 Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala  
 155 160 165  
 820 GTC CAG GGT AGC CAA TTA AAA CCG ATC CAT TAC CAT TCC CCC ATT GCT  
 Val Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala  
 170 175 180

Figure 21B



TCA GCC CAG GTA AAG TCC TGC CTG TTG CTA GCG GGG TTA ACC ACC GAG	868
Ser Ala Gln Val Lys Ser Cys Leu Leu Leu Ala Gly Leu Thr Thr Glu	185 190 195
GGG GAC ACC ACG GTT ACA GAA CCA GCT CTA TCC CGG GAT CAT AGC GAA	916
Gly Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu	200 205 210
CGC ATG TTG CAG GCC TTT GGA GCC AAA TTA ACC ATT GAT CCA GTA ACC	964
Arg Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Ile Asp Pro Val Thr	215 220 225 230
CAT AGC GTC ACT GTC CAT GGC CCG GCC CAT TTA ACG GGG CAA CGG GTG	1012
His Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val	235 240 245
GTG GTG CCA GGG GAC ATC AGC TCG GCG GCC TTT TGG TTA GTG GCG GCA	1060
Val Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala	250 255 260
TCC ATT TTG CCT GGA TCA GAA TTG TTG GTG GAA AAT GTA GGC ATT AAC	1108
Ser Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn	265 270 275
CCC ACC AGG ACA GGG GTG TTG GAA GTG TTG GCC CAG ATG GGG GCG GAC	1156
Pro Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp	280 285 290

Figure 21C

ATT ACC CCG GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT Ile Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp 295 300 305 310	1204
CTG CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA Leu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu 315 320 325	1252
ATT ATT CCC CGA CTG ATT GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala 330 335 340	1300
GCC TTT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG Ala Phe Ala Glu Gly Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg 345 350 355	1348
GTT AAA GAA AGC GAT CGC CTG CGC GCC ATT GCT TCG GAG TTG GGC AAA Val Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys 360 365 370	1396
ATG GGG GCC AAA GTC ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG Met Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly 375 380 385 390	1444
GGA AGC CCG TTA CAA GGG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC Gly Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg 395 400 405	1492

**Figure 21D**

ATT GCC ATG GCG TTG GCG ATC GCC GCT TTA GGT AGT GGT GGT CAA ACA	1540
Ile Ala Met Ala Leu Ala Ile Ala Ala Ala Ser Gly Gly Gln Thr	
410	420
ATT ATT AAC CGG GCG GAA GCG GCC GCG ATT TCC TAT CCA GAA TTT TTT	1588
Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe	
425	435
GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG	1635
Gly Thr Leu Gly Gln Val Ala Gln Gly	
440	445
GGCGGTTTGT AAATGTTTTA CCAAGGTAGT TTGGGGTAAA GGCCCCAGCA AGTGCTGCCA	1695
GGGTAATTTA TCCGCAATG ACCAATCGGC ATGGACCCGTA TCGTTCAAAC TGGGTAATTC	1755
TCCCTTTAAT TCCTTAAAAG CTCGCTTAA ACTGCCCAAC GTATCTCCGT AATGGCGAGT	1815
GAGTAGAAGT AATGGGGCCA AACGGCGATC GCCACGGGAA ATTAAAGCCT GCATCACTGA	1875
CCACTTATAA CTTTCGGGA	1894

Figure 21E

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TTTAAAAACA ATGAGTTAAA AAATTATTTT TCTGGCACAC GCGCTTTTTT TGCATTTTTT 60
CTCCCATTTT TCCGGCACAA TAACGTTGGT TTTATAAAAG GAAATG ATG ATG ACG 115
Met Met Thr
1
AAT ATA TGG CAC ACC GCG CCC GTC TCT GCG CTT TCC GGC GAA ATA ACG 163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr
5 10 15
ATA TGC GGC GAT AAA TCA ATG TCG CAT CGC GCC TTA TTA TTA GCA GCG 211
Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala
20 25 30 35
TTA GCA GAA GGA CAA ACG GAA ATC CGC GCG TTT TTA GCG TGC GCG GAT 259
Leu Ala Glu Gly Gln Thr Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp
40 45 50
TGT TTG GCG ACG CCG CAA GCA TTG CGC GCA TTA GGC GTT GAT ATT CAA 307
Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln
55 60 65
AGA GAA AAA GAA ATA GTG ACG ATT CGC GGT GTG GGA TTT CTG GGT TTG 355
Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu
70 75 80

```

Figure 22A

CAG CCG CCG AAA GCA CCG TTA AAT ATG CAA AAC AGT GGC ACT AGC ATG	403
Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met	
85 90 95	
CGT TTA TTG GCA GGA ATT TTG GCA CCG CAG CGC TTT GAG AGC GTG TTA	451
Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu	
100 105 110 115	
TGC GGC GAT GAA TCA TTA GAA AAA CGT CCG ATG CAG CGC ATT ATT AC	499
Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr	
120 125 130	
CCG CTT GTG CAA ATG GGG GCA AAA ATT GTC AGT CAC AGC AAT TTT AC	547
Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr	
135 140 145	
GCG CCG TTA CAT ATT TCA GGA CCG CCG CTG ACC GGC ATT GAT TAC GCG	595
Ala Pro Leu Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala	
150 155 160	
TTA CCG CTT CCC AGC GCG CAA TTA AAA AGT TGC CTT ATT TTG GCA GGA	643
Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly	
165 170 175	
TTA TTG GCT GAC GGT ACC ACC GCG CTG CAT ACT TGC GGC ATC AGT CGC	691
Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg	
180 185 190 195	

Figure 22B

GAC CAC ACG GAA CGC ATG TTG CCG CTT TTT GGT GGC GCA CTT GAG ATC	739
Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile	210
200	
205	
AAG AAA GAG CAA ATA ATC GTC ACC GGT GGA CAA AAA TTG CAC GGT TGC	787
Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu His Gly Cys	225
215	
220	
GTG CTT GAT ATT GTC GGC GAT TTG TCG GCG GCG GCG TTT TTT ATG GTT	835
Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Phe Phe Met Val	240
230	
235	
GCG GCT TTG ATT GCG CCG CGC GCG GAA GTC GTT ATT CGT AAT GTC GGC	883
Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Ile Arg Asn Val Gly	255
245	
250	
ATT AAT CCG ACG CGG CGC GCA ATC ATT ACT TTG TTG CAA AAA ATG GGC	931
Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln Lys Met Gly	275
260	
265	
GGA CGG ATT GAA TTG CAT CAT CAT CAG CGC TTT TGG GGC GCC GAA CCG GTG	979
Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala Glu Pro Val	290
280	
285	
GCA GAT ATT GTT GTT TAT CAT TCA AAA TTG CGC GGC ATT ACG GTG GCG	1027
Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala	305
295	
300	

Figure 22C

CCG GAA TGG ATT GCC AAC GCG ATT GAT GAA TTG CCG ATT TTT TTT ATT	1075
Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile	
310 315 320	
GCG GCA GCT TGC GCG GAA GGG ACG ACT TTT GTG GGC AAT TTG TCA GAA	1123
Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu	
325 330 335	
TTG CGT GTG AAA GAA TCG GAT CGT TTA GCG GCG ATG GCG CAA AAT TTA	1171
Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Gln Asn Leu	
340 345 350 355	
CAA ACT TTG GGC GTG GCG TGC GAC GTT GGC GCC GAT TTT ATT CAT ATA	1219
Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe Ile His Ile	
360 365 370	
TAT GGA AGA AGC GAT CCG CAA TTT TTA CCG GCG GTG AAC AGT TTT	1267
Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe	
375 380 385	
GCG GAT CAT CCG ATT GCG ATG AGT TTG GCG GTG GCA GGT GTG CGC GCG	1315
Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala	
390 395 400	
GCA GGT GAA TTA TTG ATT GAT GAC GGC GCG GTG GCG GCG GTT TCT ATG	1363
Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met	
405 410 415	

Figure 22D

CCG CAA TTT CGC GAT TTT GCC GCC GCA ATT GGT ATG AAT GTA GGA GAA	1411
Pro Gln Phe Arg Asp Phe 425	
420	
AAA GAT GCG AAA AAT TGT CAC GAT TGATGGTCCT AGCGGTGTG GAAAAGGCAC	1465
Lys Asp Ala Lys Asn Cys His Asp	
440	
GGTGGCGCAA GCTT	1479

Figure 22E



PG2982	1	MS	HSASPKPATA	RRSEALTGEI	RRSEALTGEI	RIPGDKSISH	40
LBAA		MS	HSASPKPATA	RRSEALTGEI	RRSEALTGEI	RIPGDKSISH	
Agrobacterium CP4		MS	HGASSRPATA	RKSSGLSGTV	RKSSGLSGTV	RIPGDKSISH	
Synechocystis sp. PCC6803		MALLSLNNHQ	SHORLTVNPP	AQGVALTGRL	AQGVALTGRL	RVPGDKSISH	
B. subtilis		.....MKR	DKVQTLHGEI	HIPGDKSISH	HIPGDKSISH	HIPGDKSISH	
D. nodosus		..MMTNIWHT	APVSALSGEI	TICGDKSMTH	TICGDKSMTH	TICGDKSMTH	
S. aureus		..MVNEQII	DISGPKLGEI	EVPGDKSMTH	EVPGDKSMTH	EVPGDKSMTH	
Consensus		-----	-----L-G--	-I-GDKS--H	-I-GDKS--H	-I-GDKS--H	
PG2982	41	RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	GEDVINTGRA	MQAMGAKI.R	80
LBAA		RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	GEDVINTGRA	MQAMGAKI.R	
Agrobacterium CP4		RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	GEDVINTGRA	MQAMGAKI.R	
Synechocystis sp. PCC6803		RALMLGAIAT	GETIIEGLLL	GEDPRSTAHC	GEDPRSTAHC	FRAMGAEISE	
B. subtilis		RSVMFGALAA	GTTTVKNFLP	GADCLSTIDC	GADCLSTIDC	FRKMGVHI.E	
D. nodosus		RALLLAALAE	GQTEIRGFLL	CADCLATRQA	CADCLATRQA	LRLGVDI.Q	
S. aureus		RAIMLASLAE	GVSTIYKPLL	GEDCRRTMDI	GEDCRRTMDI	FRHLGVEI.K	
Consensus		R--MF---A- G---	I---L-	--D---T---	--D---T---	---MG---I---	
PG2982	81	KEGDVWIING	VNGCCLLQPE	AALDFGNAGT	AALDFGNAGT	GARLTMGLVG	120
LBAA		KEGDVWIING	VNGCCLLQPE	AALDFGNAGT	AALDFGNAGT	GARLTMGLVG	
Agrobacterium CP4		KEGDTWIIDG	VNGGGLLQPE	APLDFGNAAT	APLDFGNAAT	GCRLTMGLVG	
Synechocystis sp. PCC6803		LNSEKIIVQG	RGLGQLQEPS	TVLDAGNSGT	TVLDAGNSGT	TMRMLGLLA	
B. subtilis		QSSSDVVIHG	KGIDALKEPE	SLLDVGNST	SLLDVGNST	TIRMLGLILA	
D. nodosus		REKEIVTIRG	VGFLGLQPPK	APLNMQNSGT	APLNMQNSGT	SMRLLAGILA	
S. aureus		EDDEKLVVTS	PGYQ.VNTPH	QVLYTGNSGT	QVLYTGNSGT	TTRLLAGLLS	
Consensus		-----I-- -G-----P-	--L---N--T	--RL--G---	--RL--G---	--RL--G---	

Figure 23A

PG2982	121	TY.DMKTSFI	GDASLSKRPM	GRVLNPLREM	GVQVEAADGD	160
LBAA		TY.DMKTSFI	GDASLSKRPM	GRVLNPLREM	GVQVEAADGD	
Agrobacterium CP4		VY.DFDSTFI	GDASLTKRPM	GRVLNPLREM	GVQVKSEDDG	
Synechocystis sp. PCC6803		GQKDCFLT	VTGDDSLRHRPM	SRVIQPLQQM	GAKIWARNSG	
B. subtilis		G.RPFYSAVA	GDESIKRPM	KRVTEPLKKM	GAKIDGRAGG	
D. nodosus		AQR.FESVLC	GDESLEKRPM	QRIITPLVQM	GAKIVSHSNF	
S. aureus		GLGN.ESVLS	GDVSIKRPM	DRVLRPLKLM	DANIEGIEDN	
Consensus		-----	GD-S---RPM	-RV--PL--M	---I-----	
PG2982	161	RMPLTLIGPK	TANPITYRVP	MASQVKSASV	LLAGLNTPGV	200
LBAA		RMPLTLIGPK	TANPITYRVP	MASQVKSASV	LLAGLNTPGV	
Agrobacterium CP4		RLPVTLRGPK	TPTPITYRVP	MASQVKSASV	LLAGLNTPGI	
Synechocystis sp. PCC6803		KFAPLAVQGS	QLKPIHYHSP	IASAQVKSCL	LLAGLTTEGD	
B. subtilis		EFTPLSVSGA	SLKGIDYVSP	VASQIKSASV	LLAGLQAEET	
D. nodosus		T.APLHISGR	PLTGIDYALP	LPSAQLKSCL	ILAGLLADGT	
S. aureus		.YTPLIHKPS	VIKGINYQME	VASQVKSASV	LFASLFSKEP	
Consensus		-----	----I-Y---	--SAO-KS--	-LA-L-----	
PG2982	201	TTVIEPVMTR	DHTEKMLQGF	....GADLT	VETDKDGVRRH	240
LBAA		TTVIEPVMTR	DHTEKMLQGF	....GADLT	VETDKDGVRRH	
Agrobacterium CP4		TTVIEPIMTR	DHTEKMLQGF	....GANLT	VETDADGVRT	
Synechocystis sp. PCC6803		TTVTEPALSR	DHSERMLQAF	....GAKLT	IDPVTHSV..	
B. subtilis		TTVTEPHKSR	DHTERMLSAF	....GVKLS	EDQT...SV..	
D. nodosus		TRLHTCGISR	DHTERMLPLF	....GGALE	IKK..EQI..	
S. aureus		TIKELDVSR	NHTETMFKHF	NIPIEAEGLS	INTTPEAIRY	
Consensus		T-----R	-H-E-ML--F	-----L-	-----V--	

Figure 23B

PG2982	241	IRITGQGLV	GQTIDVPGDP	SSTAFPLVAA	LLVEGSDVTI	280
LBAA		IRITGQGLV	GQTIDVPGDP	SSTAFPLVAA	LLVEGSDVTI	
Agrobacterium CP4		IRLEGRGKLT	GQVIDVPGDP	SSTAFPLVAA	LLVPGSDVTI	
Synechocystis sp. PCC6803		.TVHGPAGLT	GQRVVVPGDI	SSAAFVLAAG	SILPGSELLV	
B. subtilis		.SIAGGQKLT	AADIFVPGDI	SSAAFFLAAG	AMVPNSRIVL	
D. nodosus		.IVTGGQKLH	GCVLDIVGDL	SAAAFFMVAA	LIAPRAEVVI	
S. aureus		IKPAD.....	...FHVPGDI	SSAAFFIVAA	LITPGSDVTI	
Consensus		-----	-----V-GD-	S--AF-----	-----	
PG2982	281	RNVLMNPTRT	GLILTLQEMG	ADIEVLNARL	AGGEDVADLR	320
LBAA		RNVLMNPTRT	GLILTLQEMG	ADIEVLNARL	AGGEDVADLR	
Agrobacterium CP4		LNVLMPNTRT	GLILTLQEMG	ADIEVINPRL	AGGEDVADLR	
Synechocystis sp. PCC6803		ENVGINPTRT	GVLEVLQMG	ADITPENERL	VTGEPVADLR	
B. subtilis		KNVGLNPTRT	GIIDVLQNMG	AKLEIKPSAD	SGAEPYGDLI	
D. nodosus		RNVGINPTRA	AIITLLQKMG	GRIELHHQRF	WGAEPVADIV	
S. aureus		HNVGINQTRS	GIIDIVEKMG	GNIQLFNQT.	TGAEPASIR	
Consensus		-NV--N-TR-	-----MG	-----	---E-----	
PG2982	321	VR.ASKLKGV	VPPERAPSM	IDEYPVLAIA	ASFAEGETVM	360
LBAA		VR.ASKLKGV	VPPERAPSM	IDEYPVLAIA	ASFAEGETVM	
Agrobacterium CP4		VR.SSTLKGV	TVPEDRAPSM	IDEYPILAVA	AAFAEGATVM	
Synechocystis sp. PCC6803		VR.ASHLQGC	TFGGEIIPRL	IDEIPILAVA	AAFAEGTTRI	
B. subtilis		IE.TSSLKAV	EIGGDIIPRL	IDEIPIIALL	ATQAEGETTVI	
D. nodosus		VY.HSKLRGI	TVAPEWIANA	IDELPIFFIA	AACAEGTTFV	
S. aureus		IQYTPMLQPI	TIEGELVPKA	IDELPVIALL	CTQAVGTSTI	
Consensus		V-----L---	-----E-----	IDE-PI----	---A-G-----	

Figure 23C

361	PG2982	DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	400
	LBAA	DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	
	Agrobacterium CP4	NGLEELRVKE	SDRLSAVANG	LKLVGVDCDE	GETSLVVGR	
	Synechocystis sp. PCC6803	EDAAELRVKE	SDRLAAIASE	LKMGAKVTE	FDDGLEIQGG	
	B. subtilis	KDAAELRVKE	TNRIDTVVSE	LRKLGAIEP	TADGMKVYK	
	D. nodosus	GNLSELRVKE	SDRLAAMAQN	LQTLGVACDV	GADFIHIYGR	
	S. aureus	KDAEELRVKE	TNRIDTTADM	LNLLGFELQP	TNDGLIIHPS	
	Consensus	----EL-VKE	--R-----	L---G-----	-----V---	
401	PG2982	PDGKGLG...	GGTVATHLDH	RIAMSFVLMG	LAAEKPVTVD	440
	LBAA	PDGKGLG...	GGTVATHLDH	RIAMSFVLMG	LAAEKPVTVD	
	Agrobacterium CP4	PDGKGLGNAS	GAAVATHLDH	RIAMSFVLMG	LVSENPVTVD	
	Synechocystis sp. PCC6803	SPLQ.....	GAEVDSLTDH	RIAMALIAAA	LGSGGQTIIN	
	B. subtilis	QTLK.G....	GAAVSSHGDH	RIGMMLGIAS	CITEEPIEIE	
	D. nodosus	SDRQFL....	PARVNSFGDH	RIAMSLAVAG	VRAAGELLID	
	S. aureus	E.....FK	TNATDILTTH	RIGMMLAVAC	VLSSPEVKIK	
	Consensus	-----	-----DH	RI-M-L-V--	-----I-	
441	PG2982	DSNMIATSFP	EFMDMMPGLG	AKIELSIL..	...	473
	LBAA	DSNMIATSFP	EFMDMMPGLG	AKIELSIL..	...	
	Agrobacterium CP4	DATMIATSFP	EFMDLMAGLG	AKIELSDTKA	A..	
	Synechocystis sp. PCC6803	RAEAAAIISYP	EFFGTLGQVA	QG*.....	...	
	B. subtilis	HTDAIHVSYP	TFEHLNKLK	KKS.....	...	
	D. nodosus	DGAVAAVSMF	QFRDFAAAIG	MNVGEKDAKN	CHD	
	S. aureus	QFDAVNVSFP	GFLPKLLQ	NEG.....	...	
	Consensus	-----S-P	-F-----	-----	---	

Figure 23D

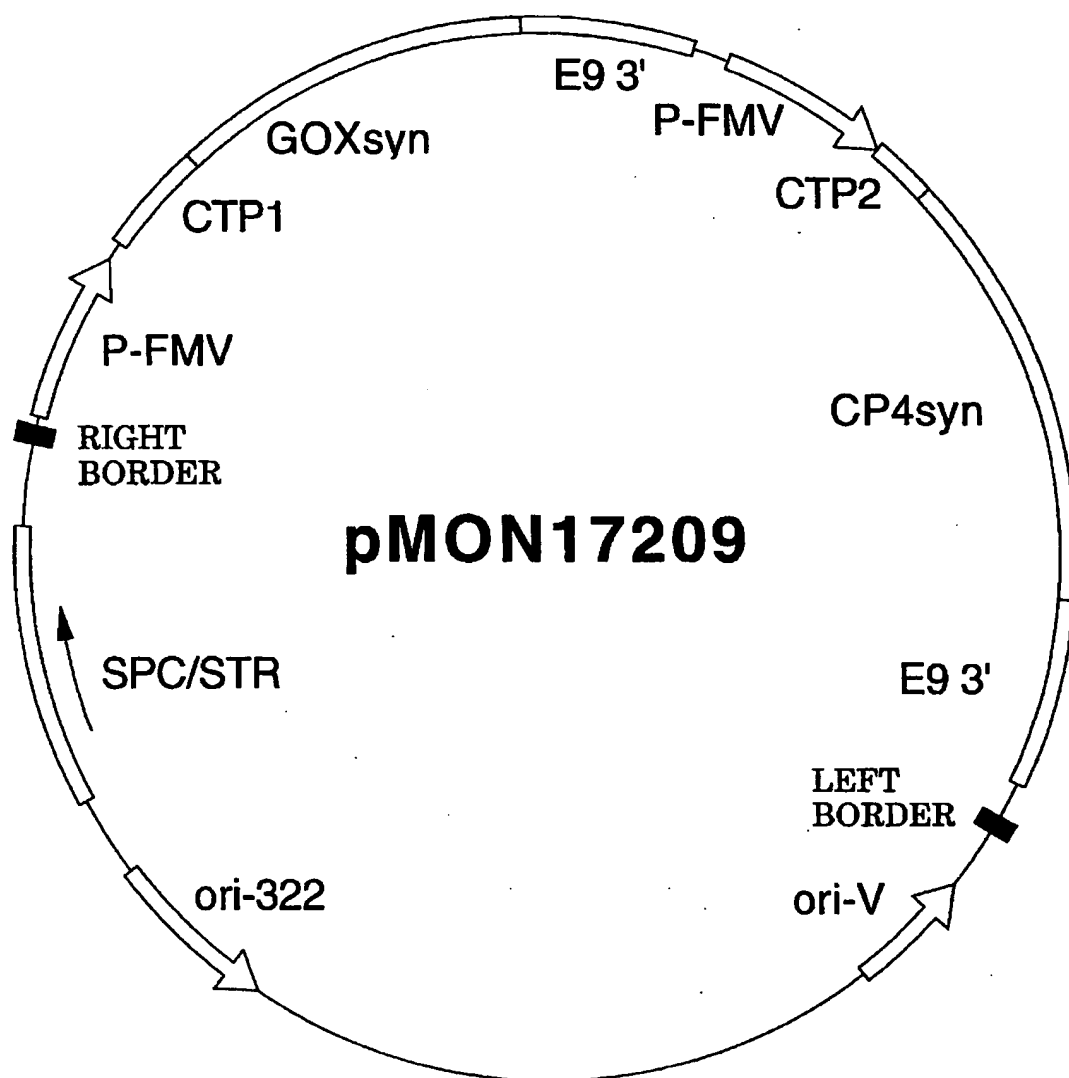


Figure 24

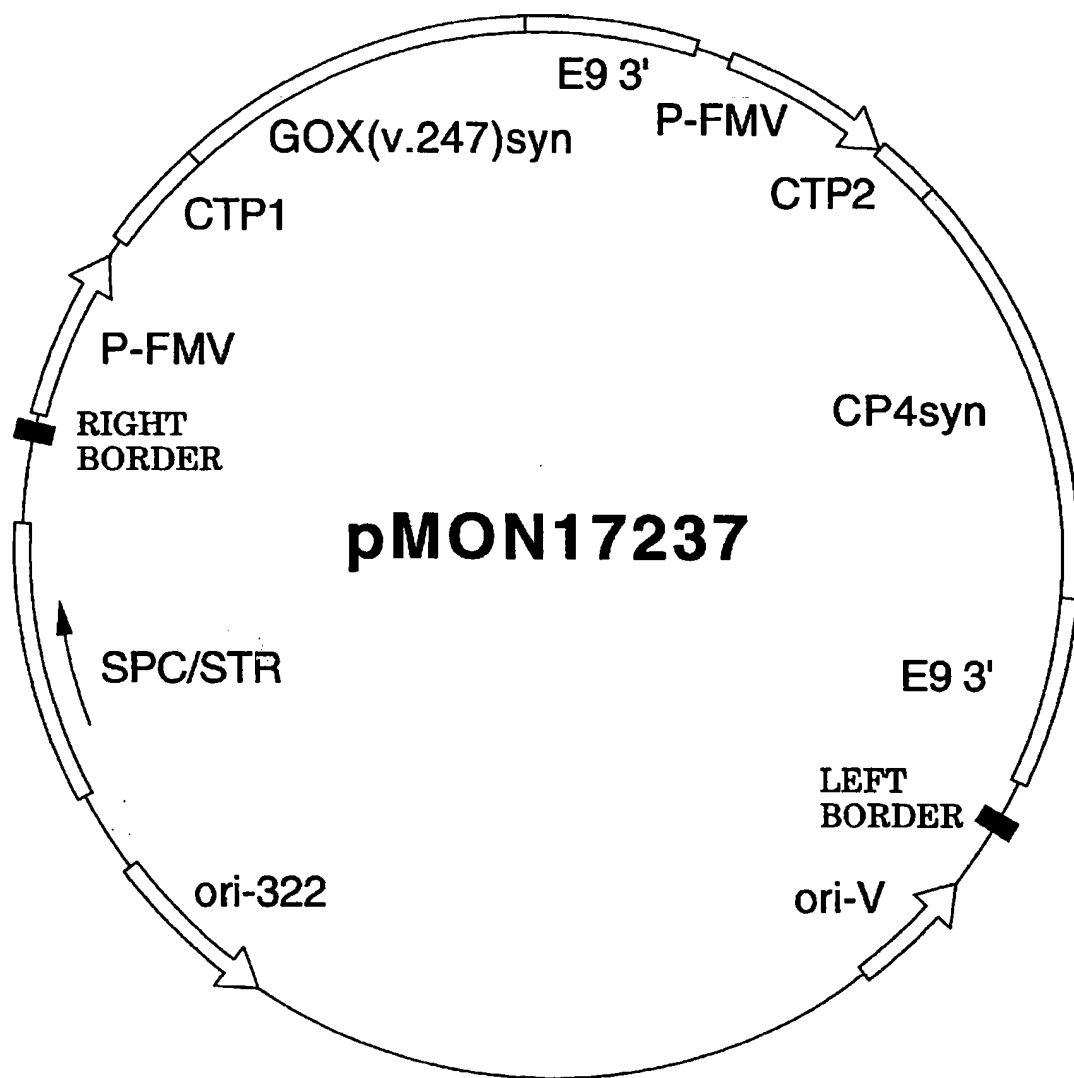


Figure 25